

HUMAN xiap

```

SEQ ID NO:3      1 gaaaagggtggacaagtcctaatttcaagagaagatgacttttaacagtttgaaggatct 60
                  1-----+-----+-----+-----+-----+-----+
SEQ ID NO:4 a    M T F N S F E G S -
                  61 aaacttggtacctgcagacatcaataaggaagaagaattttagaagagtttaataga 120
                  61-----+-----+-----+-----+-----+-----+
                  K T C V P A D I N K E E F V E E F N R -
                  121 ttaaaaacttttgctaattttccaagtggtagtcctgtttcagcatcaaacactggcacga 180
                  121-----+-----+-----+-----+-----+-----+
                  L K T F A N F P S G S P V S A S T L A R -
                  181 gcagggttcttatactgggtgaaggagataccgtgcggtgctttagttgtcatgcagct 240
                  181-----+-----+-----+-----+-----+-----+
                  A G F L Y T G E G D T V R C F S C H A A -
                  241 gtagatagatggcaatatggagactcagcagttggaagacacaggaagatcccccaat 300
                  241-----+-----+-----+-----+-----+-----+
                  V D R W Q Y G D S A V G R H R K V S P N -
                  301 tgcagatttatcaacggccttttatcttgaaaaatagtgccacgcagtcctacaaattctggt 360
                  301-----+-----+-----+-----+-----+-----+
                  C R F I N G F Y L E N S A T Q S T N S G -

```

Fig. 1A

HUMAN xiap

```

361  atccagaatggtcagtacaaagttagaaaactatctgggaagcagagatcatttgcctta 420
a    I Q N G Q Y K V E N Y L G S R D H F A L -
361  gacaggccatctgagacacatgcagactatcttttgagaactgggcagggtttagatatata 480
a    D R P S E T H A D Y L L R T G Q V V D I -
361  tcagacaccatatacccgaggaaaccctgccatgtattgtgaagaagctagattaaagtcc 540
a    S D T I Y P R N P A M Y C E E A R L K S -
361  ttccagaactggccagactatgctcacctaaccccaagagagtagcaagtgctggactc 600
a    F Q N W P D Y A H L T P R E L A S A G L -
361  tactacacagggtattggtgaccaagtgcaagtgccttttgcgttggaactgaaaaaat 660
a    Y Y T G I G D Q V Q C F C C G K L K N -
361  tgggaacctgtgatcgtgcctggtcagaacacaggcacactttcctaattgcttctttt 720
a    W E P C D R A W S E H R R H F P N C F F -

```

Fig. 1B

HUMAN xiap

```

721      gttttggccggaatcttaattcgaagtgaatctgatgctgtgagttctgataggaat 780
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      V L G R N L N I R S E S D A V S S D R N -
      781      ttcccaaatcaacaaatcttccaagaaatcccatccatggcagattatgaagcacggatc 840
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      F P N S T N L P R N P S M A D Y E A R I -
      841      ttacttttgggacatggatatactcagttaacaaggagcagcttgcaagagctggattt 900
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      F T F G T W I Y S V N K E Q L A R A G F -
      901      tatgcttttaggtgaaggtagataaagtaaagtgccttctcactgtggaggagggtactgat 960
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      Y A L G E G D K V K C F H C G G G L T D -
      961      tggaagcccagtgagacccttgggacaacacatgctaaatggtatccagggtgcaaatat 1020
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      W K P S E D P W E Q H A K W Y P G C K Y -
      1021      ctgttagaacagaagggacaagaatatataaacaatatcttacttaactcattcacttgag 1080
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      L L E Q K G Q E Y I N N I H L T H S L E -

```

Fig. 1C

HUMAN xiap

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1081      gagtgctggtgaagaactactgagaaaaacaccatcactaactagaagaattgatgatacc 1140
      -----+-----+-----+-----+-----+-----+-----+
a      E C L V R T T E K T P S L T R R I D D T -
      -----+-----+-----+-----+-----+-----+-----+
1141      atcttccaaaatcctatggtacaagaagctatacgaaatggggttcagtttcaaggacatt 1200
      -----+-----+-----+-----+-----+-----+-----+
a      I F Q N P M V Q E A I R M G F S F K D I -
      -----+-----+-----+-----+-----+-----+-----+
1201      aagaaaataatggaggaaaaaattcagatatctgggagcaactataaactcacttgaggtt 1260
      -----+-----+-----+-----+-----+-----+-----+
a      K K I M E E K I Q I S G S N Y K S L E V -
      -----+-----+-----+-----+-----+-----+-----+
1261      ctggttgcagatctagtgaatgctcagaaagacagtatgcaagatgagtcagtcagact 1320
      -----+-----+-----+-----+-----+-----+-----+
a      L V A D L V N A Q K D S M Q D E S S Q T -
      -----+-----+-----+-----+-----+-----+-----+
1321      tcattacagaaagagattagtagtgaagagcagctaaggcgccctgcaagaggagaagctt 1380
      -----+-----+-----+-----+-----+-----+-----+
a      S L Q K E I S T E E Q L R R L Q E E K L -
      -----+-----+-----+-----+-----+-----+-----+
1381      tgcaaaaatctgtatggatagaaaatttgctatcgttttgttccttgggacatctagtc 1440
      -----+-----+-----+-----+-----+-----+-----+

```

Fig. 1D

HUMAN xiap

```

a      C K I C M D R N I A I V F V P C G H L V      -
      1441 acttgtaaacaaatgtgctgaagcagttgacaagtgccccatgtgctacacagtcattact 1500
      T C K Q C A E A V D K C P M C Y T V I T      -
      1501 ttcaagcaaaaaatttttatgtctttaaactctatagtaggcattgttatgtgttct 1560
      F K Q K I F M S *      -
      1561 tattaccctgattgaatgtgtgatgtgaactgactttaagtaatcaggattgaattcccat 1620
      tagcatttgctaccaagtaggaaaaaaatgtacatggcagtggttttagttggcaatata 1680
      atctttgaatttcttgatttttccagggtattagctgtattatccattttttttactgtta 1740
      ttttaattgaaccatagactaagaataagaagcatcatactataactgaacacaatgtgt 1800

```

Fig. 1E

HUMAN xiap

```

1801 attcatagtatactgatttaatttctaagtgtgaagtgaattaatcatctggatttttat 1860
      -----+-----+-----+-----+-----+
a      -

1861 tcttttcagataggcttaacaaaatggagctttctgtatataaatgtggagattagagtta 1920
      -----+-----+-----+-----+-----+
a      -

1921 atctcccaatcacataaattgttttgtgtgaaaaaggaaataaaattgttccatgctggtg 1980
      -----+-----+-----+-----+-----+
a      -

1981 gaaagatagagattgttttagaggttggttgtgtgttttaggattctgtccattttctt 2040
      -----+-----+-----+-----+-----+
a      -

2041 tgtaagnnataaacacgnacntgtgcgaaataatnttgtaaagtgatttgccattnttg 2100
      -----+-----+-----+-----+-----+
a      -

2101 aaagcgtatttaatgatagaatactatcgagccaacatgtactgacatggaaagatgtca 2160
      -----+-----+-----+-----+-----+
a      -

```

Fig. 1F

HUMAN xiao

2161
nagatatgttaagtgtaaaatgcaagtggcnnnacactatgtatatgtctgagccagatca 2220

॥

aagtatgtagttnntaataatgcataagaacnanagatttggaaagatatatacaccaaactg
2221-----+-----+-----+-----+-----+ 2280

॥

2281 ttaaatgtggtttctcttcgggaggggggatcgggggggcccccagaggggttta
2340

॥

2341 nagggcctttcactttcnactttttcattttgttctgttcgnattttttataagtat 2400

॥

gtanacccnaagggttttatggnaactaacatcagtaacccccgtgactatcct
-----+-----+-----+-----+-----+-----+
2401
2402

18

gtnctcttccctaggagctgtnttgttccccaccacaccttcctctgaacaaatgc
-----+-----+-----+-----+-----+-----+-----+
2461 2520

8

2521 ctgagtgcctgggcactttn 2540

10

Fig. 1G

HUMAN hiap-1

```
SEQ ID NO:5      1      TCCTTGAGATGATCAGTATAGGATTAGGATCTCCATGTTGGAAGTCTAAATGCATAGA 60
-----+-----+-----+-----+-----+-----+-----+
c
61      AATGGAAATAATGGAAATTTTTCATTTTGGCTTTTCAGCCTAGTATTAAACTGATAAAA 120
-----+-----+-----+-----+-----+-----+-----+
c
121     GCAAAGCCATGCACAAAACCTACCTCCCTAGAGAAAGGCTAGTCCCTTTTCTTCCCCATTC 180
-----+-----+-----+-----+-----+-----+-----+
c
181     ATTCATTATGAACATAGTAGAAAACAGCATATTCTTATCAAAATTGATGAAAAGCGCCA 240
-----+-----+-----+-----+-----+-----+-----+
SEQ ID NO:6      M N I V E N S I F L S N L M K S A N -
241     ACACGTTTGAACCTGAAATACGACTTGTGTCATGTGAACTGTACCGAATGTCTACGTATCCA 300
-----+-----+-----+-----+-----+-----+-----+
c
T F E L K Y D L S C E L Y R M S T Y S T -
301     CTTTCCCTGCTGGGGTTCCTGTCTCAGAAAGGAGTCTTGCTCGTGGTTCATTACA 360
-----+-----+-----+-----+-----+-----+-----+
c
F P A G V P V S E R S L A R A G F Y Y T -
```

Fig. 2A

HUMAN hiap-1

```

361      CTGGTGTGAATGACAAGGTCAAATGCTTCTGTGTGGCCTGATGCTGGATAACTGGAAAA 420
      -----+-----+-----+-----+-----+-----+-----+
      G V N D K V K C F C C G L M L D N W K R -

421      GAGGAGACAGTCTACTGAAAAGCATAAAAAGTTGTATCCTAGCTGCAGATTCGTTTCAGA 480
      -----+-----+-----+-----+-----+-----+-----+
      G D S P T E K H K K L Y P S C R F V Q S -

481      GTCTAAATTCCGGTTAAACAACCTGGAAAGCTACCTCTCAGCCCTACTTTCTTCTTCAGTAA 540
      -----+-----+-----+-----+-----+-----+-----+
      L N S V N N L E A T S Q P T F P S S V T -

541      CACATTCCACACACTCATTACTTCCGGGTACAGAAAACAGTGGATATTCCGGTGGCTCTT 600
      -----+-----+-----+-----+-----+-----+-----+
      H S T H S L L P G T E N S G Y F R G S Y -

601      ATTCAAACTCTCCATCAAATCCCTGTAAACTCCAGAGCAAATCAAGAATTTCTGCCTTGA 660
      -----+-----+-----+-----+-----+-----+-----+
      S N S P S N P V N S R A N Q E F S A L M -

661      TGAGAAGTTCCTACCCCTGTCCAATGAATAACGAAAATGCCAGATTACTTACTTTTCAGA 720
      -----+-----+-----+-----+-----+-----+-----+
      R S S Y P C P M N N E N A R L L T F Q T -

```

Fig. 2B

HUMAN hiap-1

```

721 CATGGCCATTGACTTTTCTGTCGCCAACAGATCTGGCAGCAGGCTTTACTACATAG 780
-----+-----+-----+-----+-----+
C W P L T F L S P T D L A R A G F Y Y I G -

781 GACCTGGAGACAGAGTGGCTTGCTTTGCCCTGTGGTGGAAAATTGAGCAATTGGGAACCGA 840
-----+-----+-----+-----+-----+
C P G D R V A C F A C G G K L S N W E P K -

841 AGGATAATGCTATGTCAGAACACCTGAGACATTTTCCCAAATGCCCATTTATAGAAAATC 900
-----+-----+-----+-----+-----+
C D N A M S E H L R H F P K C P F I E N Q -

901 AGCTTCAAGACACTTCAAGATACACAGTTTCTAACTCTGAGCATGCAGACACATGCAGCCCC 960
-----+-----+-----+-----+-----+
C L Q D T S R Y T V S N L S M Q T H A A R -

961 GCTTTAAACATTCTTTAACTGGCCCTCTAGTGTCTAGTTAATCCTGAGCAGCTTGCAA 1020
-----+-----+-----+-----+-----+
C F K T F F N W P S S V L V N P E Q L A S -

1021 GTGCGGGTTTATTATGTGGGTAACAGTGATGATGTCAAATGCTTTTGCTGTGATGGTG 1080
-----+-----+-----+-----+-----+
C A G F Y Y V G N S D D V K C F C C D G G -

```

Fig. 2C

HUMAN hiap-1

```

1081 GACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGTTCAACATGCCAAGTGTTCCAA 1140
-----+-----+-----+-----+-----+-----+
C L R C W E S G D D P W V Q H A K W F P R -

1141 GGTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTTCATCCGTCAAGTTCAAGCCAGTT 1200
-----+-----+-----+-----+-----+-----+
C C E Y L I R I K G Q E F I R Q V Q A S Y -

1201 ACCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCAGGAGATGAAATGCAG 1260
-----+-----+-----+-----+-----+-----+
C P H L L E Q L L S T S D S P G D E N A E -

1261 AGTCATCAATTATCCATTGGAACTGGAGAAGACCATTTCAGAAGATGCAATCATGATGA 1320
-----+-----+-----+-----+-----+-----+
C S S I I H L E P G E D H S E D A I M M N -

1321 ATACTCCTGTGATTAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCCTGGTAAACAGA 1380
-----+-----+-----+-----+-----+-----+
C T P V I N A A V E M G F S R S L V K Q T -

1381 CAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAAATTATAGACTAGTCAATGATCTTGTGT 1440
-----+-----+-----+-----+-----+-----+
C V Q R K I L A T G E N Y R L V N D L V L -

```

Fig. 2D

Fig. 2E

HUMAN hiap-1

```

1801  ATGTTTCAGATCTACCAAGTGGAAACAATTGCGGAGACTACCAGAAGAAACAATGTA 1860
      V S D L P V E E Q L R R L P E E R T C K -
1861  AAGTGTGTATGGACAAAGAAGTGTCCATAGTGTATTTCCTTGTGGTCATCTAGTAGTAT 1920
      V C M D K E V S I V F I P C G H L V V C -
1921  GCAAAGATTGTGCTCCTTCTTTAAGAAAGTGTCCCTATTGTAGAGTACAATCAAGGGTA 1980
      K D C A P S L R K C P I C R S T I K G T -
1981  CAGTTCGTACATTCTTTTCATGAAGAAGAACCAAAACATCGTCTAAACTTTAGAAATTAAT 2040
      V R T F L S *
2041  TTATTAAATGTATTATAACTTTTAACTTTTATCCTAAATTGGTTTCCTTAAATTTTATT 2100
      TATTACAACCTCAAAAACAATTGTTTGTGTGAACATATTTATATATATGTATCTAAACCATA 2160

```

Fig. 2F

HUMAN hiap-1

```

2161  TGAACATATATTTTGAAGAACTAAGAGAATGATAGGCTTTTGTCTTATGACGAAAAA 2220
      -
      c

2221  GAGTAGCACTACAAACACAATATTCAATCCAAATTTCAGCATTTATTGAAATTGTAAGTG 2280
      -
      c

2281  AAGTAAAACTTAAGATATTGAGTTAACCTTTAAGAATTTTAAATATTTTGGCATTGTAC 2340
      -
      c

2341  TAATACCGGGAACAATGAAGCCAGGTGTGGTGGTAIGTACCTGTAGTCCCAGGCTGAGGCA 2400
      -
      c

2401  AGAGAAATTACTTGAGCCAGGAGTTTGAATCCATCCTGGGCAGCATACTGAGACCCCTGCC 2460
      -
      c

2461  TTTAACAAACXAAACAGXACCXAAAXCCAAACACCAGGGACACATTTCTGTCTTTTGTGAT 2520
      -
      c

```

Fig. 2G

U

2

Fig. 2H

2641 AAAAAAAAAAAAACTCAGGGCCCGTACCAAT 2676
-----+-----+-----+-----

HUMAN hiap-2

```

SEQ ID NO:7          1  TTAGGTTACCTGAAAGAGTTACTACAACCCCAAGAGTTGTGTTCTAAGTAGTATCTTGG  60
a  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
                                     -
      61  TAATTCAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAAAATCCAGTAAAGAAAG  120
a  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
                                     -
      121  TGTAGTAAATTCTACATAAGAGTCTATCATTTGATTTCTTTTGTGGTGGAAATCTTAGTT  180
a  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
                                     -
      181  CATGTGAAGAAATTTCAATGTGAATGTTTGTAGCTATCAAAACAGTACTGTACCTACTCATG  240
a  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
                                     M
      241  CACAAACTGCCCTCCCAAGACTTTTCCAGGTCCTCGTATCAAAACATTAAAGAGTATA  300
a  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      301  ATGGAAGATAGCAGATCTTGTGTCAGATTGGACAAACAGCAACAAACAAATGAAGTAT  360
a  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      M E D S T I L S D W T N S N K Q K M K Y

```

Fig. 3A

HUMAN hiap-2

```

361      GACTTTTCCTGTGAACCTCTACAGAATGCTACATATTCAACTTCCCCCGGGGTGCCT 420
      -----+-----+-----+-----+-----+-----+-----+
a      D F S C E L Y R M S T Y S T F P A G V P -
      -----+-----+-----+-----+-----+-----+-----+
421      GTCTCAGAAAGGAGTCTTGCTCGTGGTGGTTTATTATATACTGGTGTGAATGACAAGTC 480
      -----+-----+-----+-----+-----+-----+-----+
a      V S E R S L A R A G F Y Y T G V N D K V -
      -----+-----+-----+-----+-----+-----+-----+
481      AAATGCTTCTGTGGCCTGATGCTGGATAACTGGAACCTAGGAGACAGTCCTATTCAA 540
      -----+-----+-----+-----+-----+-----+-----+
a      K C F C C G L M L D N W K L G D S P I Q -
      -----+-----+-----+-----+-----+-----+-----+
541      AAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTTCAGAATCTGGTTTCAGCTAGTCTG 600
      -----+-----+-----+-----+-----+-----+-----+
a      K H K Q L Y P S C S F I Q N L V S A S L -
      -----+-----+-----+-----+-----+-----+-----+
601      GGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTTCACATTATCTCTCCC 660
      -----+-----+-----+-----+-----+-----+-----+
a      G S T S K N T S P M R N S F A H S L S P -
      -----+-----+-----+-----+-----+-----+-----+
661      ACCTTGGAACATAGTACTTGTTCAGTGGTCTTACTCCAGCCTTCCTCCAAACCCCTCTT 720
      -----+-----+-----+-----+-----+-----+-----+
a      T L E H S S L F S G S Y S S L P P N P L -

```

Fig. 3B

HUMAN hiap-2

```

721  AATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAATG 780
      N S R A V E D I S S S R T N P Y S Y A M -
      AGTACTGAAGAAGCCAGATTCTTCTTACCTACCATATGTGGCCATTAACTTTTGTGCACCA 840
781  -----+-----+-----+-----+-----+-----+-----+
      S T E E A R F L T Y H M W P L T F L S P -
      TCAGAATTGGCAAGAGCTGGTTTTTATTATATAGGACCTGGAGATAGGGTAGCCTGCTTT 900
841  -----+-----+-----+-----+-----+-----+-----+
      S E L A R A G F Y Y I G P G D R V A C F -
      GCCTGTGGTGGGAAGCTCAGTAACTGGGAACCAAGAGATGATGCTATGTCAGAACACCCGG 960
901  -----+-----+-----+-----+-----+-----+-----+
      A C G G K L S N W E P K D D A M S E H R -
      AGGCATTTCCCAACTGTCCATTTTGGAAAATTCTCTAGAAACTCTGAGGTTAGCATT 1020
961  -----+-----+-----+-----+-----+-----+-----+
      R H F P N C P F L E N S L E T L R F S I -
      TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTATGTACTGGCCATCT 1080
1021 -----+-----+-----+-----+-----+-----+-----+
      S N L S M Q T H A A R M R T F M Y W P S -

```

Fig. 3C

HUMAN hiap-2

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1081 AGTGTTCAGTTCAGCCTGAGCAGCTTGCAAGTCTGGTGTGTTTATTATGTGGTTCGCAAT 1140
      S V P V Q P E Q L A S A G F Y Y V G R N -
1141 GATGATGTCAAATGCTTTGGTTGTGATGGTGGCTTGAGGTGTGGGAATCTGGAGATGAT 1200
      D D V K C F G C D G G L R C W E S G D D -
1201 CCATGGGTAGAAACATGCCAAGTGTTCCAAAGGTGTGAGTCTTGTGATACGAATGAAAGGC 1260
      P W V E H A K W F P R C E F L I R M K G -
1261 CAAGAGTTTGTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGCTGTGTGCA 1320
      Q E F V D E I Q G R Y P H L L E Q L L S -
1321 ACTTCAGATACCACTGGAGAAGAAAATGCTGACCCCAATATTATTTGGACCTGGA 1380
      T S D T T G E E N A D P P I I H F G P G -
1381 GAAAGTTCTTCAGAAGATGCTGTGATGATGAATACACCTGTGGTTAAATCTGCCCTTGAA 1440
      E S S S E D A V M M N T P V V K S A L E -

```

Fig. 3D

HUMAN hiap-2

1441	ATGGGCTTTAATAGAGACCTGGTGAACAACAGTTCTAAGTAAATCCTGCAACTGGA	1500
a	M G F N R D L V K Q T V L S K I L T T G	-
1501	GAGAACTATAAACAGTTAATGATATTGTGTCAGCACTTCTTAATGCTGAAGATGAAAAA	1560
a	E N Y K T V N D I V S A L L N A E D E K	-
1561	AGAGAAGAGGAGGAGGAAAAACAAGCTGAAGAAATGGCATCAGATGATTTGTCATTAATT	1620
a	R E E E K E K Q A E E M A S D D L S L I	-
1621	CGGAAGAACAGAAATGGCTCTCTTTCAACAATTGACATGTGTGCTTCCTATCCTGGATAAT	1680
a	R K N R M A L F Q Q L T C V L P I L D N	-
1681	CTTTTAAAGGCCAATGTAATTAATAAACAGGAACATGATATTATTAAACAAAAACACAG	1740
a	L L K A N V I N K Q E H D I I K Q K T Q	-
1741	ATACCTTTACAAGCGAGAGAACTGATTGATACCATTGGGTTAAGGAAATGCTGCGGCC	1800
a	I P L Q A R E L I D T I W V K G N A A A	-

Fig. 3E

HUMAN hiap-2

```

1801 AACATCTTCAAAACTGTCTAAAGAAATTGACTCTACATTGTATAAGAACTTATTGTG 1860
a   N I F K N C L K E I D S T L Y K N L F V -
1861 GATAAGAAATATGAAGTATATCCACAGAAGATGTTTCAGGCTGTCTGCTGGAAGACAA 1920
a   D K N M K Y I P T E D V S G L S L E E Q -
1921 TTGAGGAGGTTGCAAGAAGAACTTGTAAGTGTGTATGGACAAAGAAGTTTCTGTT 1980
a   L R R L Q E E R T C K V C M D K E V S V -
1981 GTATTTATCCTTGTGGTCATCTGGTAGTATGCCAGGAATGTCCCTTCTCTAAGAAA 2040
a   V F I P C G H L V V C Q E C A P S L R K -
2041 TGCCCTATTGCAGGGGTATAATCAAGGGTACTGTTCTGTACATTTCTCTTAAAGAAA 2100
a   C P I C R G I I K G T V R T F L S * -
2101 ATAGTCTATATTTAACCTGCATAAAAGGCTTTAAATATTGTTGAACACTTGAAGCC 2160
a

```

Fig. 3F

HUMAN hiap-2

```

2161 ATCTAAAGTAAAAGGGAATTATGAGTTTTTCAATTAGTAACATTCATGTTCTAGTCTGC 2220
-----+-----+-----+-----+-----+-----+-----+
a

2221 TTGGTACTAATACTTGTCTGAAAGATGGTATCATATATTAACTTAATCTGTT 2280
-----+-----+-----+-----+-----+-----+-----+
a

2281 TATTACAAGGAAGATTATGTTTGTGGAACATATATTAGTATGTATGTGTACCTAAGGG 2340
-----+-----+-----+-----+-----+-----+-----+
a

2341 AGTAGGTCXCTGCTTGTATGCATCATTTCCAGGAGTACTGGATTGTGTTCTTTCAG 2400
-----+-----+-----+-----+-----+-----+-----+
a

2401 AAAGCTTGAAAXACTAAATTATAGTGTAGAAAAGAACTGGAAACCAGGAACCTCTGGAGTT 2460
-----+-----+-----+-----+-----+-----+-----+
a

2461 CATCAGATTATGGTGCCGAATTGTCTTTTGGTGCTTTTCACTTGTGTTTAAATAAGGA 2520
-----+-----+-----+-----+-----+-----+-----+
a

2521 TTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTGCTTTAAAG 2580
-----+-----+-----+-----+-----+-----+-----+
a

```

Fig. 3G

MOUSE xiap

```

SEQ ID NO:9      1      60
GACACTCTGGCGGGCGGCCCTCCTCCGGGACCTCCCTCGGGAACCGTCGCCC
-----+-----+-----+-----+-----+-----+
a

61      120
GCGGCGCTTAGGACTGGAGTGCTTGGCGCGAAAGGTGGACAAGTCCTATTTCCA
-----+-----+-----+-----+-----+-----+
a

121      180
GAGAAGATGACTTTTAACAGTTTGAAGGAAGTAACTTTTGTAAGTGCAGACCAAT
-----+-----+-----+-----+-----+-----+
M T F N S F E G T R T F V L A D T N

181      240
AAGGATGAAGAAATTTGTAGAAGAGTTTAATAGATTAAACATTGTGTAACCTCCCAAGT
-----+-----+-----+-----+-----+-----+
K D E E F V E E F N R L K T F A N F P S

241      300
AGTAGTCCTGTTTCAGCATCAACATTGGCGCGAGCTGGGTTTCTTATACCGTGAAGGA
-----+-----+-----+-----+-----+-----+
a

301      360
GACACCGTGCAATGTTTCAGTTGTGTCATGCGGCAATAGATGGCAGTATGGAGACTCA
-----+-----+-----+-----+-----+-----+
a

D T V Q C F S C H A A I D R W Q Y G D S

```

Fig. 4A

MOUSE xiap

```

361      GCTGTTGGAAGACACAGGAGAAATATCCCCAAATTGCAGATTATCAATGGTTTATTTT 420
      -----+-----+-----+-----+-----+-----+-----+
a      A V G R H R R I S P N C R F I N G F Y F -
      -----+-----+-----+-----+-----+-----+-----+
421      GAAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAAATGGCCAGTACAAATCTGAA 480
      -----+-----+-----+-----+-----+-----+-----+
a      E N G A A Q S T N P G I Q N G Q Y K S E -
      -----+-----+-----+-----+-----+-----+-----+
481      AACTGTGTGGAAATAGAAATCCTTTTGCCCTGACAGGCCACCTGAGACTCATGCTGAT 540
      -----+-----+-----+-----+-----+-----+-----+
a      N C V G N R N P F A P D R P P E T H A D -
      -----+-----+-----+-----+-----+-----+-----+
541      TATCTCTGAGAACTGGACAGGTTGTAGATATTCAGACACCATATACCCGAGGAACCT 600
      -----+-----+-----+-----+-----+-----+-----+
a      Y L L R T G Q V V D I S D T I Y P R N P -
      -----+-----+-----+-----+-----+-----+-----+
601      GCCATGTGTAGTGAAGCCAGATTGAAGTCATTCAGAACTGGCCGACTATGCTCAT 660
      -----+-----+-----+-----+-----+-----+-----+
a      A M C S E E A R L K S F Q N W P D Y A H -
      -----+-----+-----+-----+-----+-----+-----+
661      TTAACCCACAGAGTTAGCTAGTGTGGCTCTACTACACAGGGCTGATGATCAAGTG 720
      -----+-----+-----+-----+-----+-----+-----+
a      L T P R E L A S A G L Y Y T G A D D Q V -

```

Fig. 4B

MOUSE xiap

```

721 CAATGCTTTTGTGGGGAAAACTGAAAAATTGGGAACCCCTGTGATCGTGCCCTGGTCA 780
-----+-----+-----+-----+-----+-----+
a   Q C F C C G G K L K N W E P C D R A W S -
781 GAACACAGGAGACACTTCCCAATGCTTTTGTGTTTGGGCCGGAACGTTAATGTTTCA 840
-----+-----+-----+-----+-----+-----+
a   E H R R H F P N C F F V L G R N V N V R -
841 AGTGAATCTGGTGTGAGTTCTGTAGGAATTCCCAAATTCAACAACTCTCCAAGAAAT 900
-----+-----+-----+-----+-----+-----+
a   S E S G V S S D R N F P N S T N S P R N -
901 CCAGCCATGGCAGAAATATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTT 960
-----+-----+-----+-----+-----+-----+
a   P A M A E Y E A R I V T F G T W I Y S V -
961 AACAAAGGACGCTTGCAAGAGCTGGATTATTATGCTTTAGTGAAGCGGATAAAGTGAAG 1020
-----+-----+-----+-----+-----+-----+
a   N K E Q L A R A G F Y A L G E G D K V K -
1021 TGCTTCCACTGTGGAGGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAG 1080
-----+-----+-----+-----+-----+-----+
a   C F H C G G G L T D W K P S E D P W D Q -

```

Fig. 4C

MOUSE xiap

```

1081 CATGCTAAGTGCTACCCAGGTGCAAAATACCTATTGGATGAGAAGGGCAAGATATATA 1140
a   H A K C Y P G C K Y L L D E K G Q E Y I -
1141 AATAATATTCAATTAAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAAAACA 1200
a   N N I H L T H P L E E S L G R T A E K T -
1201 CCACCGCTAACTAAAAATCGATGATACCATCTTCCAGAATCCTATGGTGCAAGAAGCT 1260
a   P P L T K K I D D T I F Q N P M V Q E A -
1261 ATACGAATGGGATTAGCTTCAAGGACCTTAAGAAACAATGGAAGAAAAAATCCAAACA 1320
a   I R M G F S F K D L K K T M E E K I Q T -
1321 TCCGGGAGCAGCTATCTACTTGAGGTCTTGATTCAGAGATCTTGTGAGTGTCTCAGAAA 1380
a   S G S S Y L S L E V L I A D L V S A Q K -
1381 GATAATACGGAGGATGAGTCAAGTCAAACTTCATTGCAGAAAGACATTAGTACTGAAGAG 1440
a   D N T E D E S S Q T S L Q K D I S T E E -

```

Fig. 4D

MOUSE xiap

```

1441 CAGCTAAGGCGCCTACAAGAGGAGAAAGCTTTCCAAAATCTGTATGGATAGAAAATATTGCT 1500
-----+-----+-----+-----+-----+-----+-----+
a   Q L R R L Q E E K L S K I C M D R N I A -
    ATCGTTTTTTTCCCTTGTGGACATCTGGCCACTTGTAAACAGTGTGCAGAACGAGTTGAC 1560
-----+-----+-----+-----+-----+-----+-----+
a   I V F F P C G H L A T C K Q C A E A V D -
    AAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAAATTTTATGCTTAGTGG 1620
-----+-----+-----+-----+-----+-----+-----+
a   K C P M C Y T V I T F N Q K I F M S * -
    GGCACCACATGTTATGTTCTTCTTGTCTCTAATTGAATGTGTAATGGGAGCGAACTTTAAG 1680
-----+-----+-----+-----+-----+-----+-----+
a   TAATCCGTGCATTTCATTCCATTAGCATCCCTGCTGTTTCCAAAATGGAGACCAATGCTAAC 1740
-----+-----+-----+-----+-----+-----+-----+
a   AGCACTGTTTCCGTCCTAAACATTCAATTTCTGGATCTTTTCGAGTTATCAGCTGTATCATT 1800
-----+-----+-----+-----+-----+-----+-----+
a

```

Fig. 4E

MOUSE xiap

```

1801 TAGCCAGTGTTTACTCGATTGAACCTTAGACAGAGAAAGCATTTATAGCTTTTCACAT 1860
      -
a
1861 GTATATTGGTAGTACACTGACTTGATTCTATATGTAAGTGAATTCATCACCTGCATGTT 1920
      -
a
1921 TCATGCCTTTTGCATAAGCTTAACAAATGGAGTGTCTGTATAAGCATGGAGATGTGATG 1980
      -
a
1981 GAATCTGCCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAGAAGTCCCCACGCTG 2040
      -
a
2041 CTGGGAGGATAAAGATTGTTTATAGATGCTCACTTCTGTGTTTATAGGATTCGCCCATTTA 2100

```

Fig. 4F

M-hiap-1

```

SEQ ID NO:39      1  GAATTCGGGAGACCTACACCCCGGAGATCAGAGGTCAATTGCTGGCGTTCAGAGCCTAG 60
                   +-----+-----+-----+-----+-----+-----+
                   61  GAAGTGGGCTGCGGTATCAGCCTAGCAGTAAACCGACCAGAGCCATGCACAAACTAC 120
                   +-----+-----+-----+-----+-----+-----+
                   121 ATCCCCAGAGAAAGACTTGTCCCTTCCCTCCCTGTCACTCTCACCATGAACATGGTTCAA 180
                   +-----+-----+-----+-----+-----+-----+
                   M N M V Q -

SEQ ID NO:40      181 GACAGCGCCTTTCTAGCCAAGCTGATGAAGAGTGTGACACCTTTGAGTTGAAGTATGAC 240
                   +-----+-----+-----+-----+-----+-----+
                   D S A F L A K L M K S A D T F E L K Y D -
                   241 TTTTCCTGTGAGCTGTACCGATTGTCCACGTATTCAGCTTTTCCCAGGGGAGTTCCTGTG 300
                   +-----+-----+-----+-----+-----+-----+
                   F S C E L Y R L S T Y S A F D R G V P V -
                   301 TCAGAAAGGAGTCTGGCTCGTGGCTTTTACTACACTGGTGCCTCAATGACAAGGTCAAG 360
                   +-----+-----+-----+-----+-----+-----+
                   S E R S L A R A G F Y Y T G A N D K V K -
                   361 TGCTTCTGCTGGCCTGATGCTAGACAACTGGAAACAAGGGGACAGTCCCATGGAGAAG 420
                   +-----+-----+-----+-----+-----+-----+
                   C F C C G L M L D N W K Q G D S P M E K -

```

Fig. 5A

M-hiap-1

```

421  CACAGAAAGTTGTACCCAGCTGCAACTTTGTACAGACTTTGAATCCAGCCAACAGTCTG
      H R K L Y P S C N F V Q T L N P A N S L - 480
481  GAAGCTAGTCCTCGGCCTTCTCTCTCCACGGGATGAGCACCATGCCCTTGAGCTTT
      E A S P R P S L P S T A M S T M P L S F - 540
541  GCAAGTCTGAGAATACTGGCTATTTCAGTGGCTCTTACTCGAGCTTCCCTCAGACCCT
      A S S E N T G Y F S G S Y S S F P S D P - 600
601  GTGAACTTCCGAGCAAATCAAGATTGTCTCTGCTTTGAGCACAAGTCCCTACCACCTTGCA
      V N F R A N Q D C P A L S T S P Y H F A - 660
661  ATGAACACAGAGAAGGCCAGATTACTCACCTATGAACATGGCCATTGCTTTCTGTCA
      M N T E K A R L L T Y E T W P L S F L S - 720
721  CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGGACCTGGAGATAGAGTGGCCTGC
      P A K L A K A G F Y Y I G P G D R V A C - 780

```

Fig. 5B

M-hiap-1

```

781  TTTGCGTCCGATGGGAAACTGAGCAACTGGGAACGTAAGGATGATGCTATGTCAGAGCAC 840
    F A C D G K L S N W E R K D D A M S E H -
841  CAGAGGCATTTCCCCAGCTGTCCGTTCTTALLKACTTGGGTCAGTCTGCTTCGAGATAC 900
    Q R H F P S C P F L K D L G Q S A S R Y -
901  ACTGTCTCTAACCTGAGCATGCAGACACACGCAGCCCGTATTAGAACATTCTCTAACTGG 960
    T V S N L S M Q T H A A R I R T F S N W -
961  CCTTCTAGTGCACTAGTTCAATTCACAGGAAGTGGGCTTTTATTATACAGGA 1020
    P S S A L V H S Q E L A S A G F Y Y T G -
1021 CACAGTGATGATCAAGTGTTTATGCTGTGATGGTGGGCTGAGGTGCTGGGAATCTGGA 1080
    H S D D V K C L C C D G G L R C W E S G -
1081 GATGACCCCTGGGTGGAACATGCCAAGTGGTTTCCAAAGGTGTGAGTACTTGCTCAGAATC 1140
    D D P W V E H A K W F P R C E Y L L R I -
1141 AAAGGCCAAGAAATTTGTCAGCCCAAGTTCAGCTGGCTATCCTCATCTACTTGAGCAGCTA 1200
    K G Q E F V S Q V Q A G Y P H L L E Q L -

```

Fig. 5C

M-hiap-1

```

1201 TTATCTACGTCACTCCCCAGAAGATGAGAATGCAGACGCAGCAATCGTGCAATTTGGC 1260
      L S T S D S P E D E N A D A A I V H F G -
1261 CCTGGAGAAAGTTCGGAAGATGTCGTCAATGATGAGCAGCGCTGTGGTTAAAGCAGCCCTTG
      P G E S S E D V V M M S T P V V K A A L -
1320
1321 GAAATGGGCTTCAGTAGGAGCCCTGGTGAGACAGACGGTTCAGTGGCAGATCCTGGCCACT 1380
      E M G E S R S L V R Q T V Q W Q I L A T -
1381 GGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATGCAGAAGACGAG 1440
      G E N Y R T V S D L V I G L L D A E D E -
1441 ATGAGAGAGGAGCAGATGGAGCAGCGCGCCGAGGAGGAGAGTCAGATGATCTAGCACTA 1500
      M R E E Q M E Q A A E E E E S D D L A L -
1501 ATCCGGAAGAACAATAATGGTGCTTTTCCAACATTGACGTGTGTGACACCAATGCTGTAT 1560
      I R K N K M V L F Q Q H L T C V T P M L Y -

```

Fig. 5D

M-hiap-1

```

1561 TGCCTCCTAAGTGCAAGGGCCATCACTGAACAGGAGTGCAATGCTGTGAAACAGAAACCA
      C L L S A R A I T E Q E C N A V K Q K P - 1620
1621 CACACCTTACAAGCAAGCACACTGATTGATACTGTGTTAGCAAAAGGAAACACTGCAGCA
      H T L Q A S T L I D T V L A K G N T A A - 1680
1681 ACCTCATTCAGAAACTCCCTTCGGGAAATTGACCCCTGCGTTATACAGAGATATTTGTG
      T S F R N S L R E I D P A L Y R D I F V - 1740
1741 CAACAGGACATTAGGAGTCTTCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG
      Q Q D I R S L P T D D I A A L P M E E Q - 1800
1801 TTGCGGCCCTCCCGGAGGACAGAAATGTGTAAGTGTGTATGGACCGAGAGGTATCCATC
      L R P L P E D R M C K V C M D R E V S I - 1860
1861 GTGTTCAATCCCTGTGGCCATCTGGTCGTGTGCAAGACTGCGCTCCCTCTCTGAGGAAG
      V F I P C G H L V V C K D C A P S L R K - 1920

```

Fig. 5E

M-hiap-1

```

1921 TGTCCCATCTGTAGAGGGACCATCAAGGGCACAGTGGGCACATTTCTCTCCTGAACAAGA 1980
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      C P I C R G T I K G T V R T F L S * -

1981 CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACCTGTCACTCCAGTTCCCAT 2040
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      TCGGAACCTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACKCACAAATATATAACAT 2100
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      GAAAAACCTTTTGTCTGAAGTCAAGAAATGAATGAATTACTTATATAATAATTTAATTGGT 2160
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      TTCCTTAAAGTGCTATTGTTCCTCCAACTCAGAAAAATGTGTTTCTGTAAACATATTACA 2220
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      TACTACCTGCATCTAAAGTATTCATATATTCATATATTCAGATGTCATGAGAGAGGGTTT 2280
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      TGTCTTGTTCCTGAAAAGCTGGTTTATCATCTGATCAGCATATACCTGGCGCAACGGGCAG 2340
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      GGCTAGAATCCATGAACCAAGCTGCAAGATCTCACGCTAAATAAGGCGGAAAGATTGG 2400
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      AGAAACGAAAGGAAATCTTTCTGTCCCAATGTATACCTTCAGACTAATGACCTCTTCC 2460
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      TATCAAGCCTTCTA
2461 - - - - - + - - - - - 2474

```

Fig. 5F

M-hiap-2

SEQ ID NO:41

```

CTGTGGTGAGATCTATTGTCCAAGTGGTGAGAACTTCATCTGGAAGTTTAAGCGGTCA
1  -----+-----+-----+-----+-----+-----+
GAAATACTATTACTACTCATGGACAKRACTGTCTCCAGAGACTCGCCCAAGGTACCTTA
61 -----+-----+-----+-----+-----+-----+
CACCCRAAAACTTAAACGTATAATGGAGAAGAGACACAATCTTGTCAAATTGGACAAAGGA
121 -----+-----+-----+-----+-----+-----+
                               M E K S T I L S N W T K E -
                               180

```

SEQ ID NO:42

```

GAGCGAAGAAAAATGAAGTTTGACTTTTCGTGTGAACCTCTACCGAATGTCTACATATTC
181 -----+-----+-----+-----+-----+-----+
S E E K M K F D F S C E L Y R M S T Y S -
                               240
AGCTTTTCCAGGGAGTTCCTGTCTCAGAGAGGAGTCTGGCTCGTGGCTTTTATTA
241 -----+-----+-----+-----+-----+-----+
A F P R G V P V S E R S L A R A G F Y Y -
                               300
TACAGGTGTGAATGACAAAGTCAAGTGCTTCTGTGTGGCCCTGATGTGGATAACTGGAA
301 -----+-----+-----+-----+-----+-----+
T G V N D K V K C F C C G L M L D N W K -
                               360
ACAAGGGGACAGTCCCTGTGTTGAAAAGCACAGACAGTCTATCCAGCTGCAGCTTGTACA
361 -----+-----+-----+-----+-----+-----+
Q G D S P V E K H R Q F Y P S C S F V Q -
                               420

```

Fig. 6A

M-hiap-2

```

421  GACTCTGCTTTCAGCCAGTCTGCAGTCTCCATCTAAGAAATATGTCTCTGTGAAAAGTAG
      T L L S A S L Q S P S K N M S P V K S R -
480  -----+-----+-----+-----+-----+-----+-----+

481  ATTTGCACATTCTGTCACCTCTGGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC
      F A H S S P L E R G G I H S N L C S S P -
540  -----+-----+-----+-----+-----+-----+-----+

541  TCTTAATTCTAGAGCAGTGGGAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT
      L N S R A V E D F S S R M D P C S Y A M -
600  -----+-----+-----+-----+-----+-----+-----+

601  GAGTACAGAAGAGGCCAGATTCTTACTTACAGTATGTGGCCTTTAAGTTTCTGTCAACC
      S T E E A R F L T Y S M W P L S F L S P -
660  -----+-----+-----+-----+-----+-----+-----+

661  AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGCCCTGGAGACAGGGTGGCCTGTTT
      A E L A R A G F Y Y I G P G D R V A C F -
720  -----+-----+-----+-----+-----+-----+-----+

721  TGCCTGTGTGGAAACTGAGCAACTGGGAACCAAGGATTATGCTATGTCAGAGCACCG
      A C G G K L S N W E P K D Y A M S E H R -
780  -----+-----+-----+-----+-----+-----+-----+

```

Fig. 6B

M-hiap-2

```

781  CAGACATTTCCCACTGTCCATTCTCTGGAAAATACTTCAGAAACACAGAGGTTAGTAT 840
      R H F P H C P F L E N T S E T Q R F S I -
      -----+-----+-----+-----+-----+-----+-----+
841  ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACC 900
      S N L S M Q T H S A R L R T F L Y W P P -
      -----+-----+-----+-----+-----+-----+-----+
901  TAGTGTTCTTTCAGCCCGAGCAGCTTGCAAAGTGTGGATTCTATTACGTGGATCGCRA 960
      S V P V Q P E Q L A S A G F Y Y V D R N -
      -----+-----+-----+-----+-----+-----+-----+
961  TGATGATGTCAAGTGCCCTTTGTTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGA 1020
      D D V K C L C C D G G L R C W E P G D D -
      -----+-----+-----+-----+-----+-----+-----+
1021 CCCCTGGATAGAACACGCCAAATGGTTTCCAAAGGTGTGAGTTCTTGATACGGATGAAGGG 1080
      P W I E H A K W F P R C E F L I R M K G -
      -----+-----+-----+-----+-----+-----+-----+
1081 TCAGGAGTTTGTGATGAGATTCAAGCTAGATATCCTCACTTCTTGAGCAGCTGTTGTC 1140
      Q E F V D E I Q A R Y P H L L E Q L L S -
      -----+-----+-----+-----+-----+-----+-----+

```

Fig. 6C

M-hiap-2

```

1141  CACTTCAGACACCCAGGAGAAGAAATGCTGACCCTACAGAGACAGTGGTGCAATTTGG      1200
      -----+-----+-----+-----+-----+-----+-----+
      T S D T P G E E N A D P T E T V V H F G -
1201  CCCTGGAGAAAGTTCGAAAGATGTCGTCAATGATGAGCACGCCCTGTGGTTAAAGCAGCCTT      1260
      -----+-----+-----+-----+-----+-----+-----+
      P G E S S K D V V M M S T P V V K A A L -
1261  GGAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAGCGGCAGATCCTGGCCAC      1320
      -----+-----+-----+-----+-----+-----+-----+
      E M G F S R S L V R Q T V Q R Q I L A T -
1321  TGGTGAGAACTACAGGACCGTCAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGA      1380
      -----+-----+-----+-----+-----+-----+-----+
      G E N Y R T V N D I V S V L L N A E D E -
1381  GAGAGAGAGAGGAGAGGAAAGACAGACTGAAGAGATGGCATCAGGTGACTTATCACT      1440
      -----+-----+-----+-----+-----+-----+-----+
      R R E E E K E R Q T E E M A S G D L S L -
1441  GATTCGGAAGAATAGAAATGGCCCTCTTTCAACAGTTGACACATGTCCTTCCTATCCTGGA      1500
      -----+-----+-----+-----+-----+-----+-----+
      I R K N R M A L E Q Q L T H V L P I L D -

```

Fig. 6D

M-hiap-2

```

1501 TAATCTTCTTGAGGCCAGTGTAATTACAAAACAGGAACATGATATTATTAGACAGAAAC
      N L L E A S V I T K Q E H D I I R Q K T - 1560
1561 ACAGATACCCCTTACAAGCAAGAGAGCTTATTGACACCGTTTTAGTCAAGGGAATGCTGC
      Q I P L Q A R E L I D T V L V K G N A A - 1620
1621 AGCCAACATCTTCAAAAACCTCTCTGAAGGGAATTGACTCCACGTTATATGAAAACCTTATT
      A N I F K N S L K G I D S T L Y E N L F - 1680
1681 TGTGAAAAGAATATGAAGTATATTCCAACAGAAACGTTTCAGGCTTGTCATTGGAAGA
      V E K N M K Y I P T E D V S G L S L E E - 1740
1741 GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAAAGTGTGTATGGACAGAGAGTTTC
      Q L R R L Q E E R T C K V C M D R E V S - 1800
1801 TATTGTGTTTCATTCGTTGGTCATCTAGTAGTCTGCCAGGAATGTGCCCCCTTCTCTAAG
      I V F I P C G H L V V C Q E C A P S L R - 1860

```

Fig. 6E

M-hiap-2

```

1861 GAAGTGCCCATCTGCAGGGGGACAAATCAAGGGGACTGTGCGCACATTTCTCTCATGAGT 1920
      K C P I C R G T I K G T V R T F L S *
1921 GAAGAAATGGTCTGAAAGTATTGTTGGACATCAGAAGCTGTCAGAACAAAGAATGAACCTAC 1980
      -----+-----+-----+-----+-----+-----+
1981 TGATTTCAAGCTCTTCAGCAGGACATTCTACTCTCTTTCAAGATTAGTAATCTTGCTTTAT 2040
      -----+-----+-----+-----+-----+-----+
2041 GAAGGGTAGCATTTGTATATTAAAGCTTAGTCTGTTGCAAGGGAAGGCTATGCTGTTGAG 2100
      -----+-----+-----+-----+-----+-----+
2101 CTACAGGACTGTGCTGTTCCAGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGA 2160
      -----+-----+-----+-----+-----+-----+
2161 CTTCTTGGGATTTGGGAATTTGGGAAAGCTTTGGAATCCAGTGATGTGGAGCTCAGAAA 2220
      -----+-----+-----+-----+-----+-----+
2221 TCCTGGAACCAAGTACTCTGGTACTCAGTAGATAGGGTACCCTGTACTTCTTGGTGCTTT 2280
      -----+-----+-----+-----+-----+-----+
2281 TCCAGTCTGGGAAATAAGGAGGAATCTGCTGCTGTTAAATTTGCTGGATGTGAGAAAT 2340
      -----+-----+-----+-----+-----+-----+
2341 AGATGAAAGTGTTCGGGTGGGGCGTGCAATCAGTGTAGTGTGTCAGGGATGTATGCAG 2400
      -----+-----+-----+-----+-----+-----+
      GCCAAACACTGTGTAG
2401 -----+----- 2416

```

Fig. 6F

Alignment of BIR (Baculoviral IAP Repeats) Domains

Baculovirus
Cp_iap
Op_iap
Human
xiap
hiap1, hiap2
Mouse
m-xiap
Insect
diap

Cydia pomonella
Orgyia pseudotsugata

IAP on X chromosome
two different human IAP genes

mouse homologue of human xiap gene

Drosophila IAP gene, not clearly a homologue of xiap or hiap

Fig. 7

note on consensus:

The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence.

SEQ ID NO:11	Op_iap-1	kaarLgTYtn	WPVqf.l	leps	rMAasGFYYL	GrgDeVrCaf	CkveitnWvr	gDdpetdHkr	wapqCpFV	68
SEQ ID NO:14	Cp_iap-1	eevRlnTFek	WPVsf.l	lspe	tMAknGFYYL	GrgDeVrCaf	CkveimrWke	gEdpaadHkk	wapqCpFV	41/61
SEQ ID NO:15	diap-2	eanRLvTFkd	WPnnpn.i	lPq	aLAKAGFYI	nrlDhVkcVw	CngviakWek	nDnafeeHkr	ffpqCprV	
SEQ ID NO:16	m-xiap-1	efnRLkTFan	FPssspvsas	tLARAGFLYt	GegDtVqCFs	ChaaidrWqy	gDsavgrHrr	ispnCrFI		
SEQ ID NO:17	xiap-1	efnRLkTFan	FPsgspvsas	tLARAGFLYt	GegDtVrCFs	ChaaavdrWqy	gDsavgrHrk	vspnCrFI		
SEQ ID NO:18	hiap1-1	elyRMstYst	FPagvpvser	sLARAGFYt	GvndkVkcFC	CglmldnWkl	gDsptekHkk	lypsCrFV		
SEQ ID NO:19	hiap2-1	elyRMstYst	FPagvpvser	sLARAGFYt	GvndkVkcFC	CglmldnWkl	gDspiqkHkq	lypsCsFI		
SEQ ID NO:20	m-xiap-2	eearLksFqn	WPdyahltp	r	eLAsAGLLYt	GadDqVqCFc	CggklknWep	cDrawseHrr	hfpnCfFV	
SEQ ID NO:21	xiap-2	eearLksFqn	WPdyahltp	r	eLAsAGLLYt	GadDqVqCFc	CggklknWep	cDrawseHrr	hfpnCfFV	
SEQ ID NO:22	hiap1-2	enaRLlTFqt	WP.lflspt	dLARAGFYI	GpgDrVaCfa	CggklknWep	kDnamseHlr	hfpnCpFI		
SEQ ID NO:23	hiap2-2	eearFlTYhm	WP.lflsps	eLARAGFYI	GpgDrVaCfa	CggklknWep	kDdamseHrr	hfpnCpFI		
SEQ ID NO:24	m-xiap-3	yearIvTFgt	Wiysv..nke	qLARAGFYal	GegDkVkcFh	CgggltdWkp	sEdpwdqHak	cyPgCkYl		
SEQ ID NO:25	xiap-3	yearIvTFgt	Wiysv..nke	qLARAGFYal	GegDkVkcFh	CgggltdWkp	sEdpweqHak	wyPgCkYl		
SEQ ID NO:26	hiap1-3	haaRfkTFfn	WPssvlvnpe	qLASAGFYV	GnsDdVkcFC	CdggllrcWes	gDdpwvqHak	wfPrC Yl		
SEQ ID NO:27	hiap2-3	haaRmrTFmy	WPssvpvqpe	qLASAGFYV	GnsDdVkcFC	CdggllrcWes	gDdpwveHak	wfPrCeFl		
SEQ ID NO:28	Op_iap-2	eearLrTFae	WPrglkqrpe	eLAeAGFFYt	GqgDktrCFc	CdggllkdWep	dDapwqqHar	wydrCeYV		
SEQ ID NO:29	Cp_iap-2	eearVksFhn	WPrckmqrpe	qMAdAGFFYt	GygDntkCFY	CdggllkdWep	eDvpweqHvr	widrCaYV		
SEQ ID NO:30	diap-3	vdarLrTFtd	WPisniqpas	aLAqAGLYYq	kigDqVrCFh	Cniglrswqk	eDepwieHak	wspkCqFV		
SEQ ID NO:31	diap-1	esvRLaTFge	WPlnapvsae	dlvanGFF..	GtwmeaeCdf	ChvrldrWey	gDlvaerHrr	sspiCsmV		
SEQ ID NO:2	Consensus	---RL-TF--	WP-----	-LA-AGFY-	G--D-V-CF-	C-----W--	-D-----H--	--P-C-FV		

SEQ ID NO:12	1	cp-iap	50
SEQ ID NO:13	...	diap	...
SEQ ID NO:10	...	m-xiap	...
SEQ ID NO:4	...	xiap	...
SEQ ID NO:6	...	hiap1	...
SEQ ID NO:8	...	hiap2	...
SEQ ID NO:44	...	consensus	...
BIR 1			
51	100		
cp-iap
diap
m-xiap
xiap
hiap1
hiap2
consensus
BIR 1			
101	150		
cp-iap
diap
m-xiap
xiap
hiap1
hiap2
consensus

Fig. 8A

151	cp-iapmSD	lrl.....	EEvRLnTF	200
	diap	esDnegnsvv	dspscscpd	lll.....	..EanRLvTF	ekWPv.sfls
	m-xiap	ppEthadyll	rtgqvDiSD	tiyprnp.am	..csEEARLksF	kdWpn.pnit
	xiap	psEthadyll	rtgqvDiSD	tiyprnp.am	ycEEARLksF	qnWpdyahLt
	hiap1	anq.....EfSa	lmrssypcpM	nnEnARLlTF	qnWpdyahLt
	hiap2	avE.....DiSs	srtnpysyam	stEEARFlTY	qtwP.ltfIs
	consensus	--E-----	-----D-SD	-----M	--EEARL-TF	hmWP.ltfIs
						--WP-----L-
201	cp-iap	PetMAknGFY	YlGrSDeVrC	afCkveImrW	kegEdpaadH	250
	diap	PqaLakAGFY	YlnrldhVkc	vwCnGviakW	EkndnAfeEH	kkwaPqCPFV
	m-xiap	PrELASAGLY	YtGadDqVqC	FcCGGKLkNW	EPcDrAwSEH	kRfFPqCPrV
	xiap	PrELASAGLY	YtGigDqVqC	FcCGGKLkNW	EPcDrAwSEH	rRHFPnCfFV
	hiap1	PtDLARAGFY	YiGpgDrVaC	FaCGGKLsNW	EPkDnAmSEH	rRHFPnCfFV
	hiap2	PsELARAGFY	YiGpgDrVaC	FaCGGKLsNW	EPkDdAmSEH	lRHFPkCPFI
	consensus	P-ELA-AGFY	Y-G--D-V-C	F-CGGKL-NW	EP-D-A-SEH	rRHFPnCpFl
						-RHFP-CPFV
251	cp-iap	kgidvcgsiv	ttnniqnttt	hdtiigPahP	kyAheaARvk	300
	diap	qmgplie.fa	tgknldelgi	qpttl.Plrp	kyAcvdARlr	sFhnWPrCmk
	m-xiap	lgrnvnvrse	s.gvssdrnf	pnstnsPrNP	aMAeyeARiv	TftdWPiSnI
	xiap	lgrnlnirse	sdavssdrnf	pnstnlPrNP	sMAdyeARif	TFgtWiys..
	hiap1	enqlqdtSry	tvS.....Nl	smgtthaARfk	TFgtWiys..
	hiap2	ensl.etlrf	sis.....Nl	smgtthaARmr	TFfnWPssvl
	consensus	-----F	-----F	--S---p-NP	-MA---AR--	TFmyWPssvp
						TF--WP-S--

Fig. 8B

BIR 3		350
cp-iap	qrpeQMaDAG FFYtGyGDnt KCFyCdGGLk dWepeDvPWe	QHvrWFdrCa
diap	qpasaLaqAG LYyqkiGdqv rCFhCniGLr swqkeDEPwf	eHAKWspkCq
m-xiap	VnkeQLaRAG FYalGeGDkV KCFhCgGGLt dwkpsEDPwD	QHAKcYPgCk
xiap	VnkeQLaRAG FYalGeGDkV KCFhCgGGLt dwkpsEDPwD	QHAKWYPgCk
hiap1	VnpEQLaSAG FYYvGnsDdV KCFcCdGGLr cwesgDDPwV	QHAKWFFPrCe
hiap2	VqpEQLaSAG FYYvGRSDdV KCFgCdGGLr cwesgDDPwV	eHAKWFFPrCe
consensus	V--EQLA-AG FYY-G-GD-V KCF-C-GGL-	-W---DDPW- QHAKWFFP-C-
		351
cp-iap	YvqlvKGrDY VqkVit.....e.....
diap	FvllaKGPAY Vsevlattaa nassqpaTap aptlq.....
m-xiap	YlldeKGQeY InnIhlthp. LeEsLgrTae kt.....Ppltk
xiap	YlldegKGQeY InnIhlthp. LeEcLvrTte kt.....Psltr
hiap1	YllirirKGQeY IrqVqasypH LLEqLlTsD spgdenaess	iihlePgEdh
hiap2	FlirrmKGQeF VdeIggryph LLEqLlTsD ttgeenadpp	iihfgPgess
consensus	Yl---KGQeY ----- L-E-L--T--	-----p----
		400
		401
cp-iap	..acVLpge.
diap	..adVLmdea pakeAltLGi dggvVrnaiaq rKllssGcaF	stldeLlhDi
m-xiap	kiDdtifgnP mVqeAirMGF sfkdLkktme eKIqtsGssY	lslevLiaDL
xiap	riDdtifgnP mVqeAirMGF sfkdIKkime eKIqisGsnY	kslevLVaDL
hiap1	seDaIMmntP vInaAveMGF srsLVKgtvq rKIlatGenY	rlvndLVlDL
hiap2	seDaVMmntP vKsAleMGF nrdLVKgtvI sKIlttGenY	ktvndiVsAl
consensus	--D-V----P -V--A--MGF -----VK----	-KI---G--Y -----LV-DL
		450

Fig. 8C

```

451                                     500
cp-iap                               .....
diap                                fddagagaal Evreppe.....
m-xiap                             vsAqkDnted E.....
xiap                               vnAqkDsmqD E.....
hiap1                             lnAedEireE Ererateeke sndlllirkn rmalfqhltc vipildsilt
hiap2                             lnAedEkreE Ekekqaema sddslirkn rmalfqqltc vipildnllk
consensus                         --A----- E-----

501                                     550
cp-iap                               .....
diap                                .....
m-xiap                             .....
xiap                               .....
hiap1                             .....
hiap2                             .....
consensus                         .....

.....nttvstaa pvsepipe...
.....psapfie pcgattskaa svpipvads i pakpqaaeav
.....ssQtsL Q.....
.....ssQtsL Q.....
agiineqehd vikqktQtsL Qarelidtil vkgniaatvf rnsIqaeav
anvinkqehd iikqktQipl Qarelidtiw vkgnaaanif knclkeidst
-----Q--L Q-----

```

Fig. 8D

		Ring Zinc Finger	
551			600
cp-iap	...tki...	...Ekepq	vedskLCKIC yveEciVCFV
diap	sniskitdei	...nlsIEEEnRq	LkDarLCKVC LDeEVgVVF1
m-xiapk diStEEQLRR	LqEEkLsKIC MDrnIaIVFf
xiapk eiStEEQLRR	LqEEkLCKIC MDrnIaIVFV
hiap1	iyehlfvqqd	...ikyiptedvs	dlpVEEQLRR LpEErtCKVC MDkEVsIVFI
hiap2	lyknlfvdkn	...mkypiptedvs	glSIEEQLRR LqEErtCKVC MDkEVsVVF1
consensus	-----	-----S-EEQLRR	L-EE-LCK-C MD-EV--VF-
601			635
cp-iap	PCGHVvCaCak	CALSVdKCPM	QRkIVtSVlk vVFS.
diap	PCGHLatCnq	CAPSVanCPM	QRadIkqfvr tFLS*
m-xiap	PCGHLatCkq	CAeaVdKCPM	CytVItfngk iFMS*
xiap	PCGHLVtCkq	CAeaVdKCPM	CytVItfkqk iFMS*
hiap1	PCGHLVvCkd	CAPslrKCPi	QRstIkgtvr tFLS*
hiap2	PCGHLVvCqe	CAPslrKCPi	QRgIIkgtvr tFLS.
consensus	PCGHLV-C--	CA-SV-KCPM	QR--I-----FLS-

Fig. 8E

Alignment of RZF (Ring Zinc Finger) Domains

Baculovirus

Cp_iap
Op_iap

Human

xiap
hiap1, hiap2

Mouse

m-xiap

Insect

diap

Cydia pomonella
Orgyia pseudotsugata

IAP on X chromosome
two different human IAP genes

mouse homologue of human xiap gene

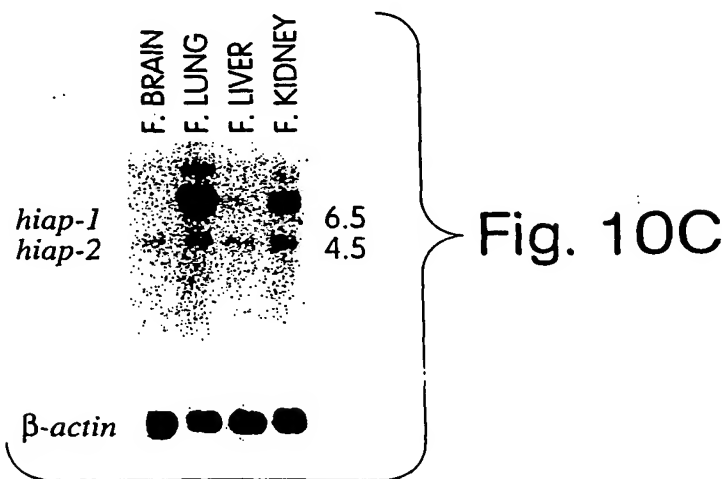
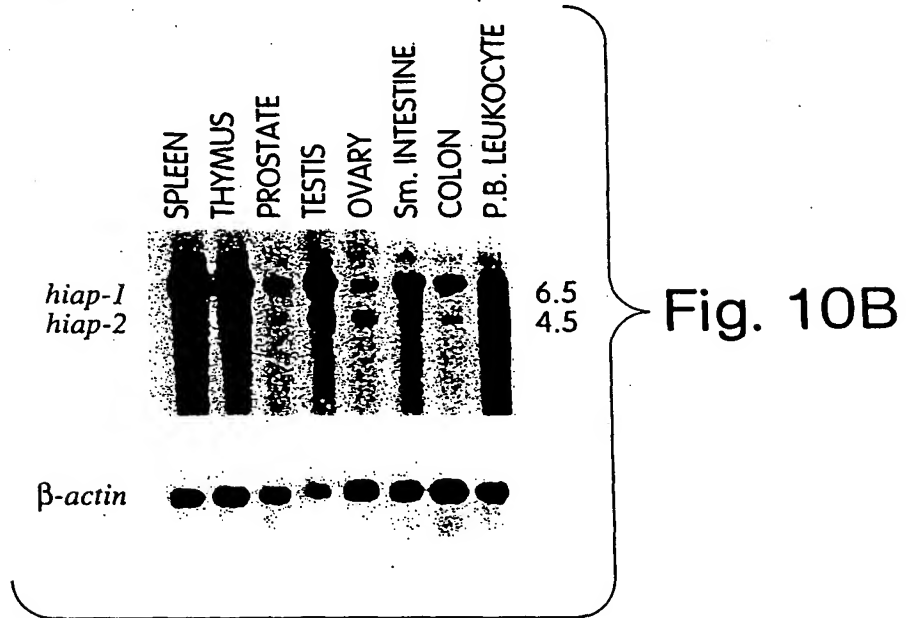
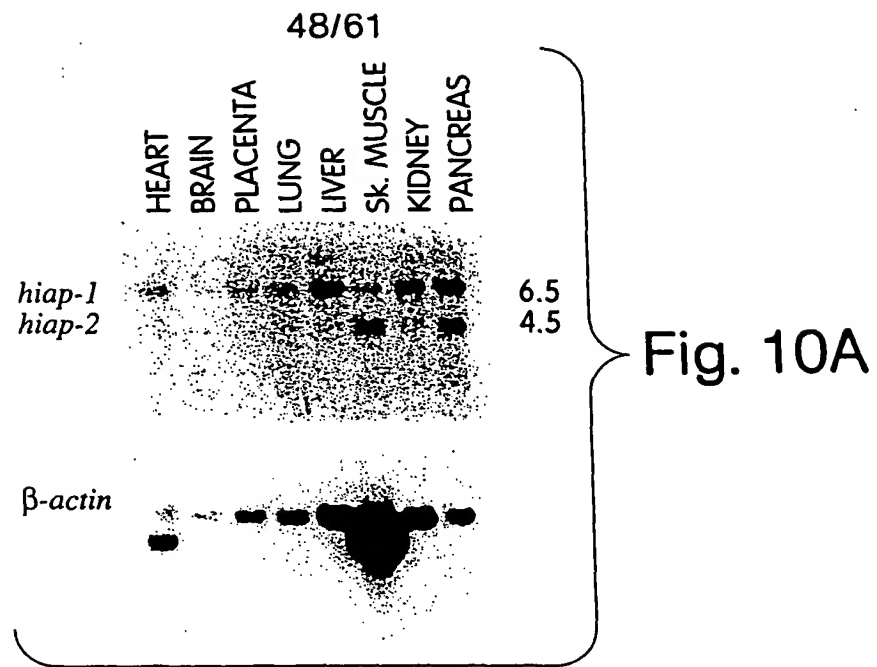
Drosophila IAP gene, not clearly a homologue of xiap or hiap

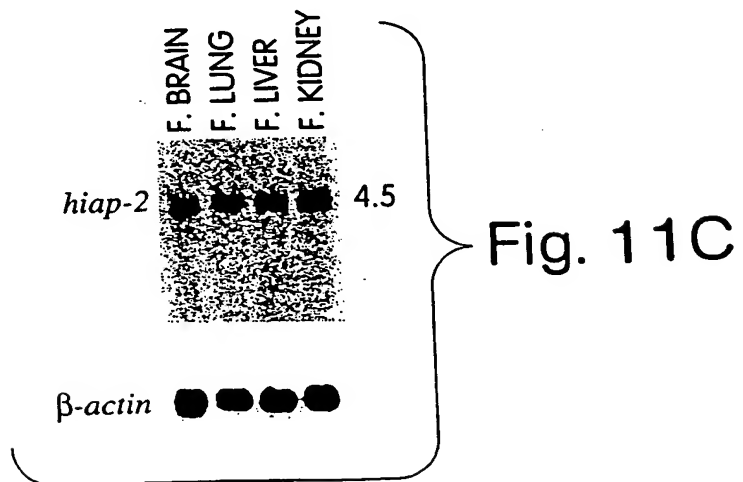
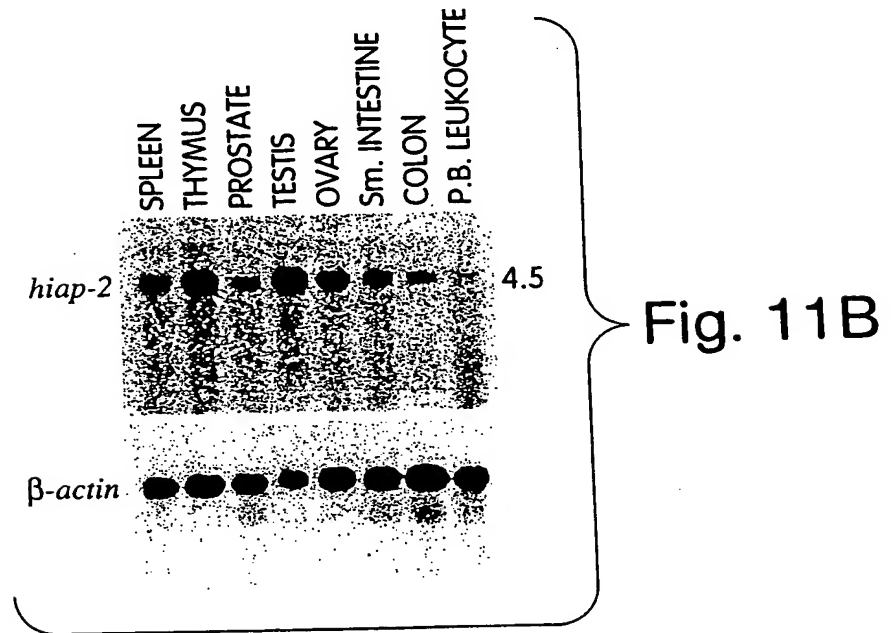
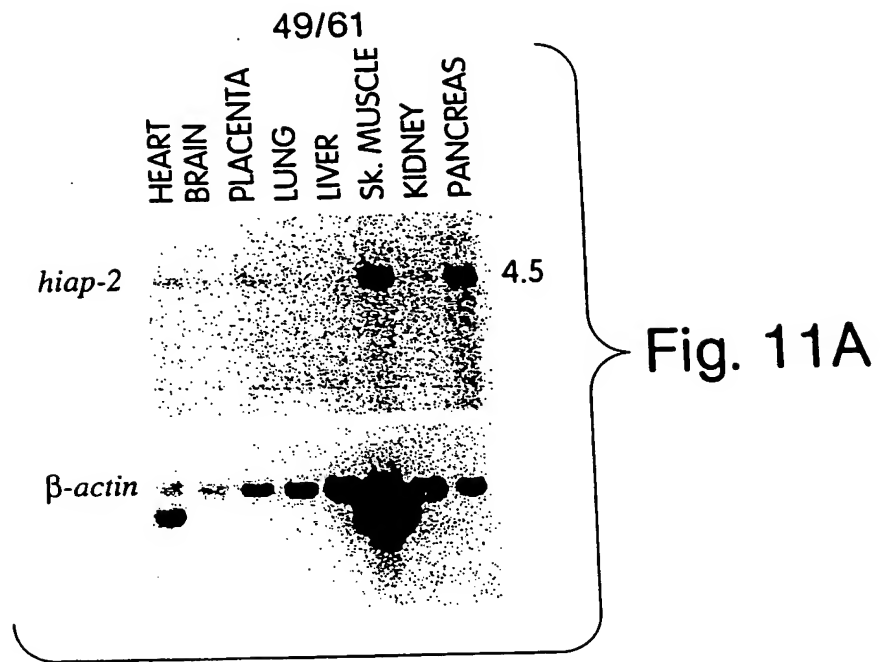
note on consensus:

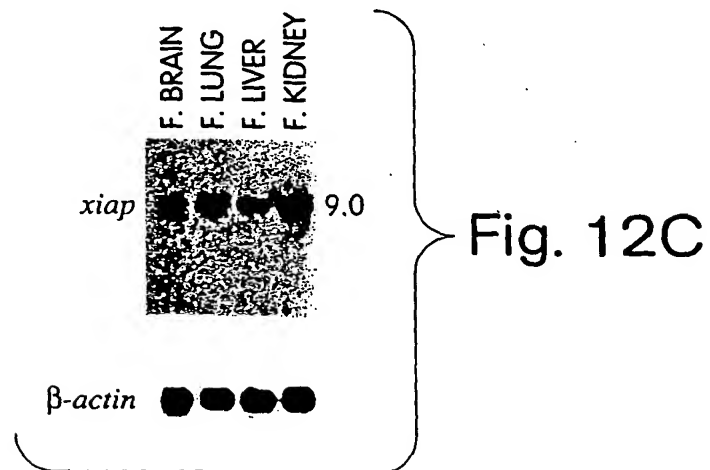
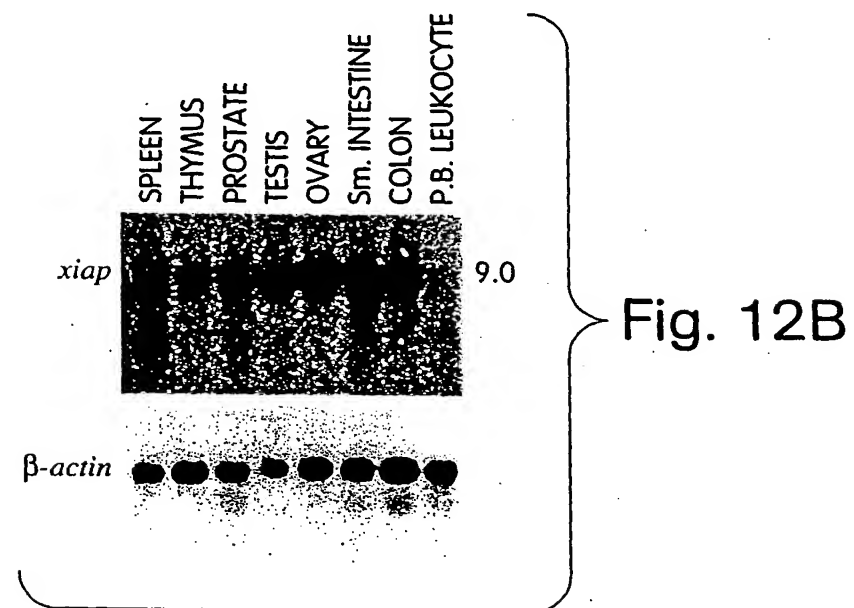
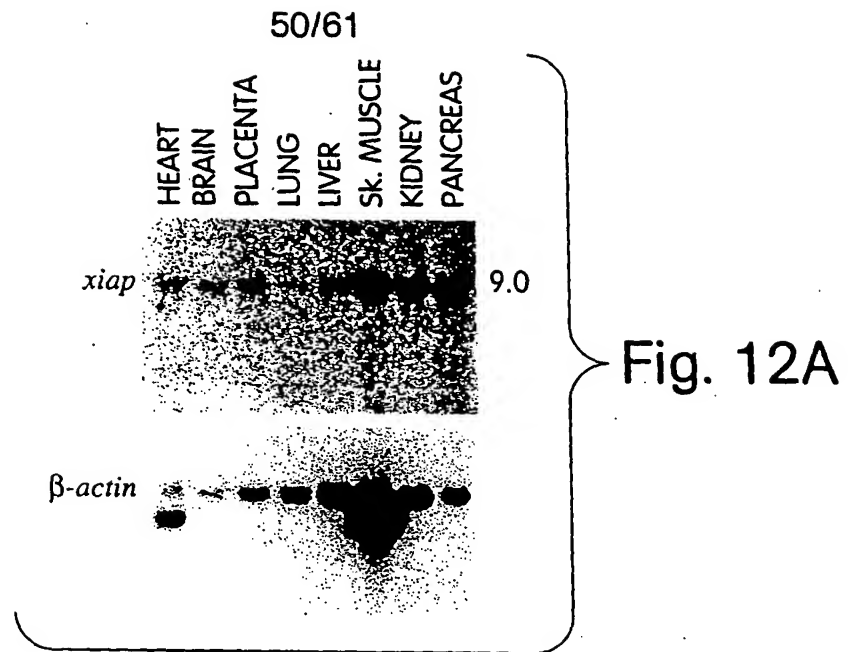
The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

SEQ ID NO:32	hiap2	1	EqlrrlqEer	tCKVCMdkev	sVvFiPCGH1	vVCqeCApel	rkCPiC	46
SEQ ID NO:33	hiap1		EqlrrlpEer	tCKVCMdkev	sIVFiPCGH1	w CkdCAPs1	rkCPiC	
SEQ ID NO:34	m-xiap		EqlrrlqEek	lSKICMdrni	aIVFfPCGH1	atCkqCAeav	dkCPmC	
SEQ ID NO:35	xiap		EqlrrlqEek	lCKICMdrni	aIVFvPCGH1	vtCkqCAeav	dkCPmC	
SEQ ID NO:36	diap		EenrqlkDar	lCKVCLdeev	gVvFlPCGH1	atCnqCApev	anCPmC	
SEQ ID NO:37	Cp_iap		EkepgveDsk	lCKICyveec	iVcFvPCGHv	vaCakCAIsv	dkCPmC	
SEQ ID NO:38	Op_iap		aveaevaDdr	lCKIClgack	tVcFvPCGHv	vaCgkCAagv	ttCPvC	
SEQ ID NO:1	consensus		E-----E--	-CKICM----	-V-F-PCGH-	--C--CA---	--CP-C	

Fig. 9







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S: STANDARDS		INCUBATION: OVERNIGHT											
		Hg			CEM-CM ₃			GT/CEM			JKT		
HIV		-	-	+	-	-	+	-	-	+	-	-	+
PHA/PMA		-	+	-	-	+	-	-	+	-	-	+	-
S		+	-	-	+	-	-	+	-	-	+	-	-

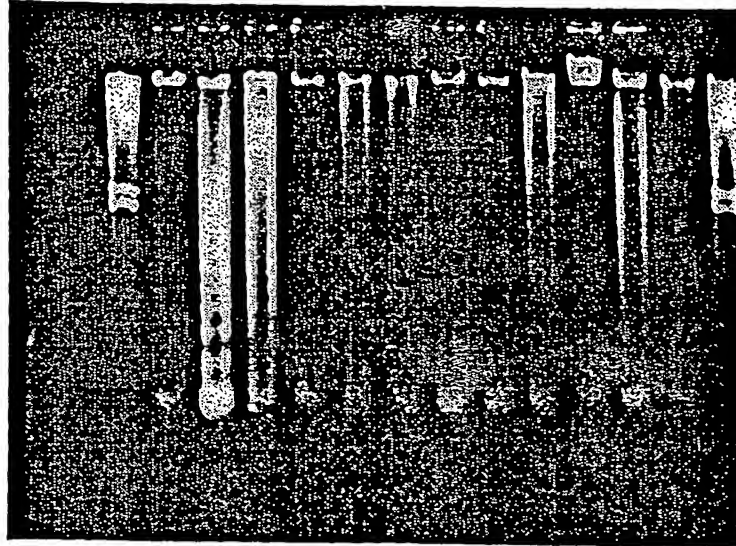


Fig. 13A

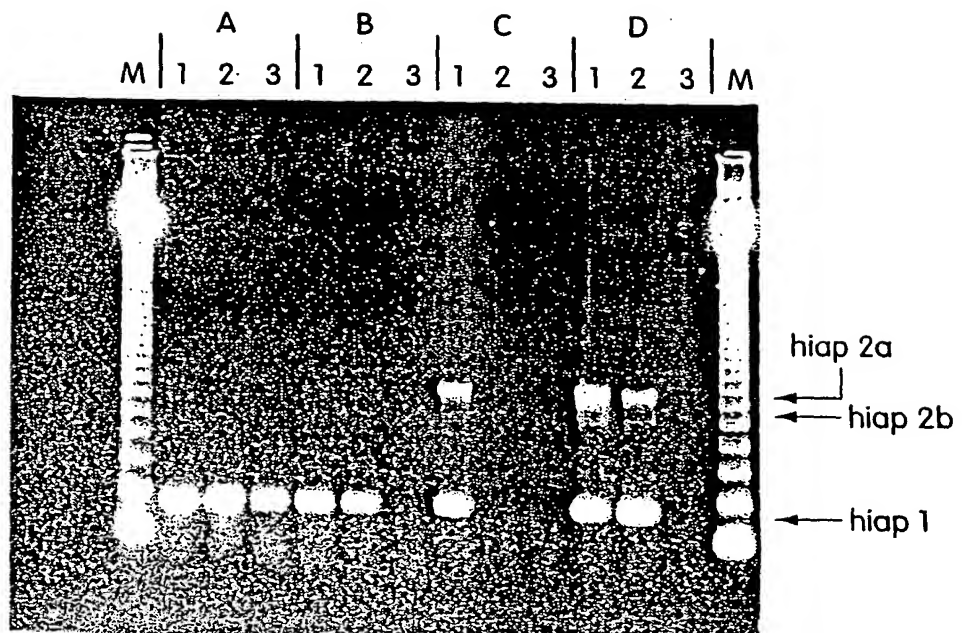


Fig. 13B

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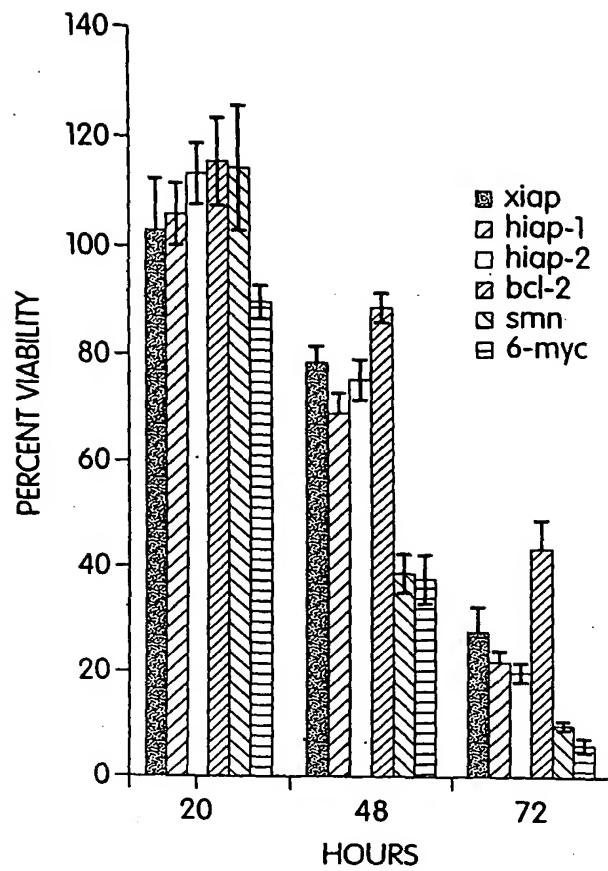


Fig. 14A

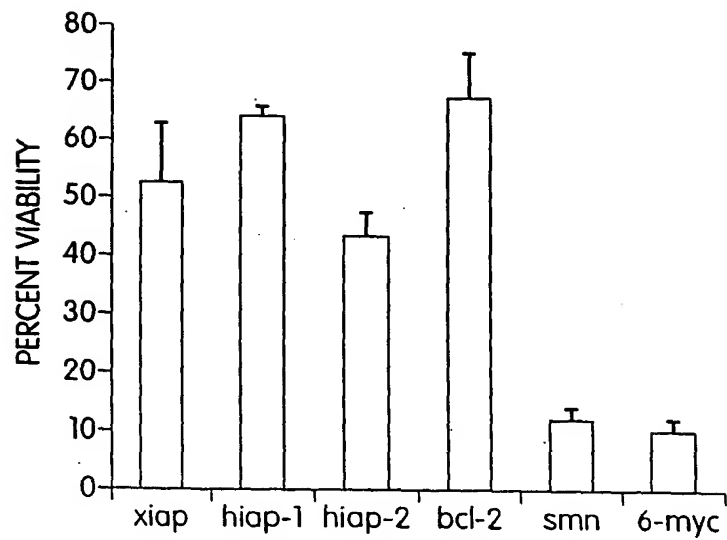


Fig. 14B

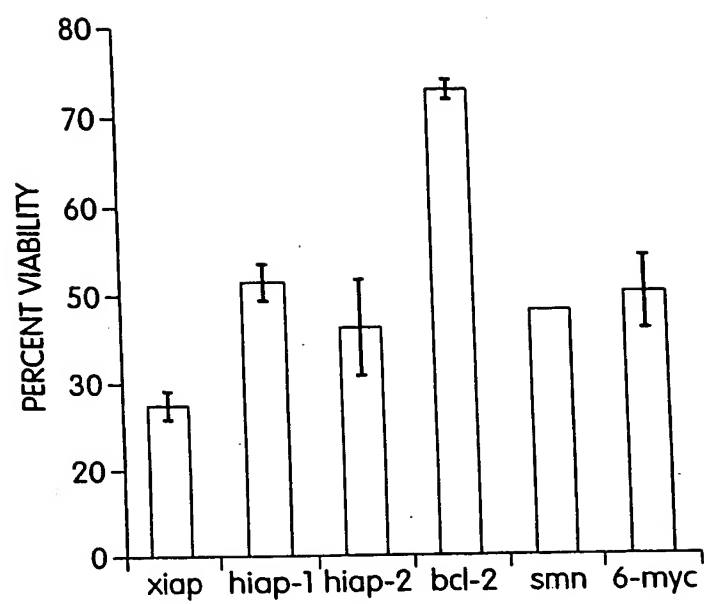


Fig. 14C

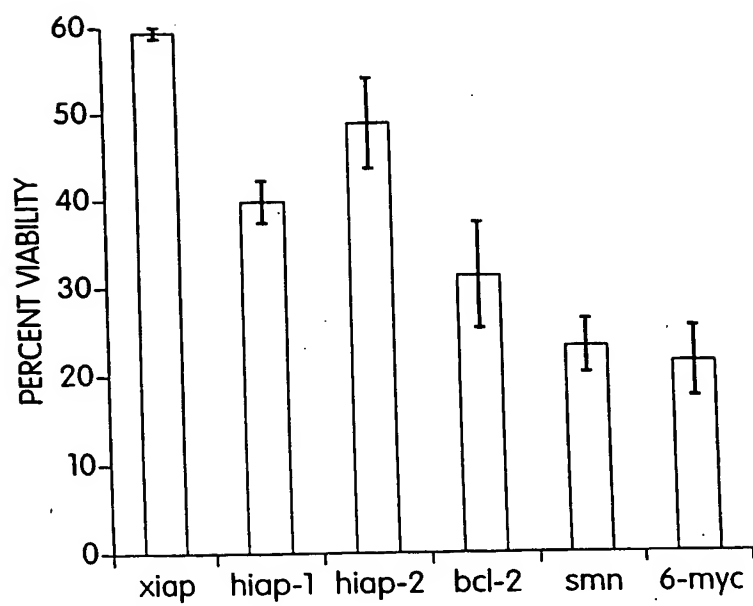


Fig. 14D

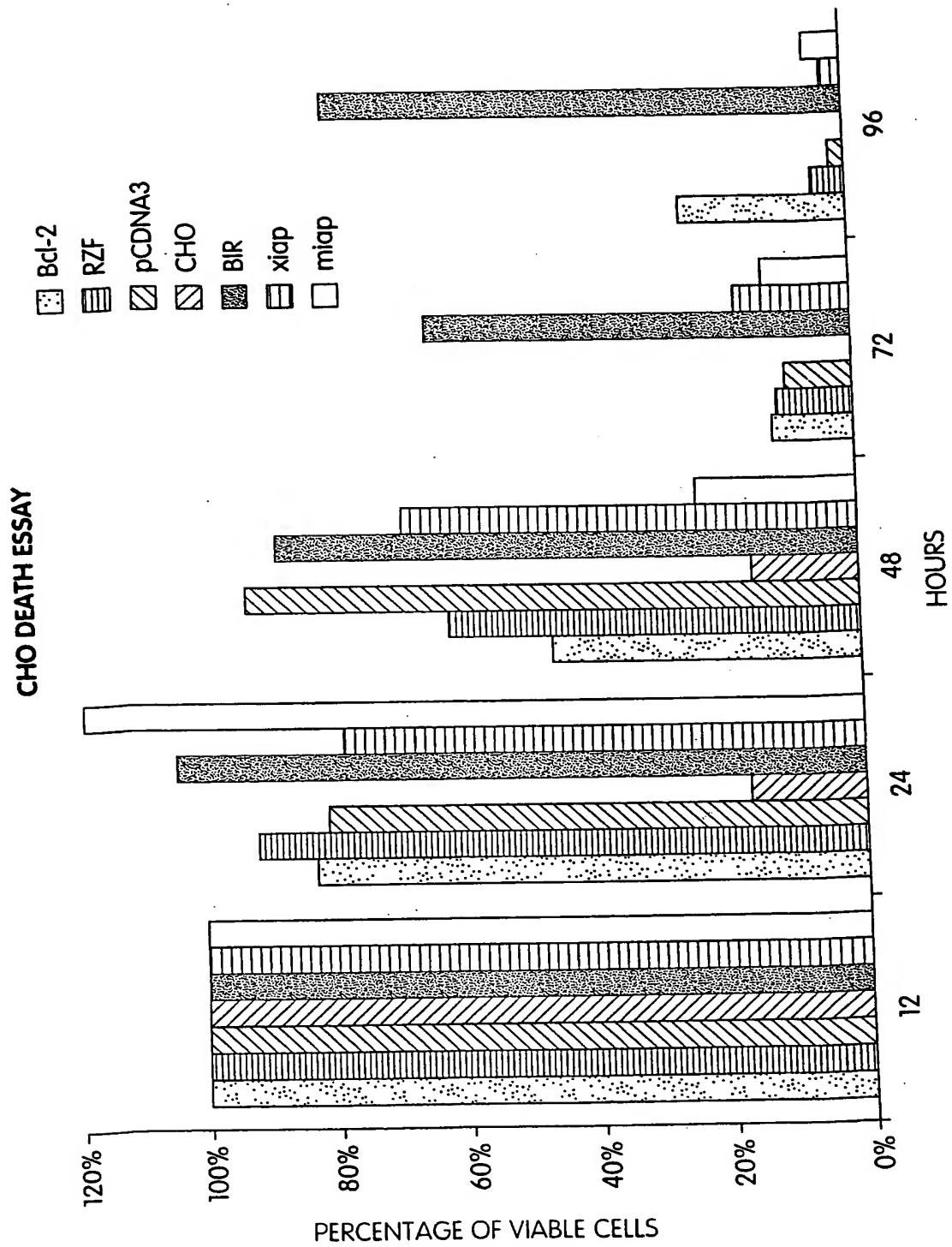
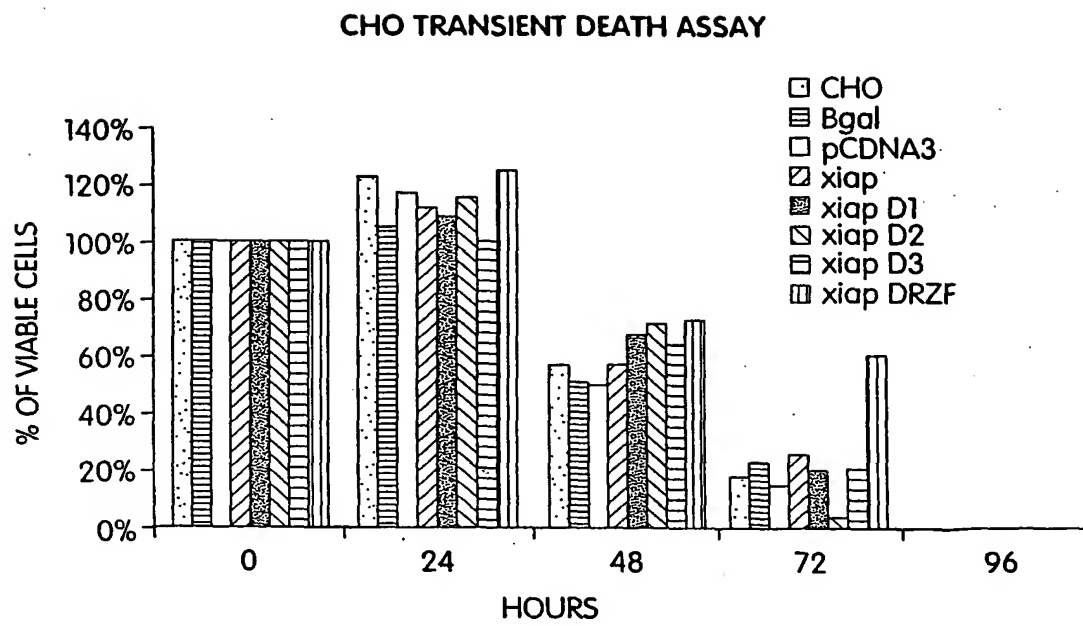


Fig. 15A

**Fig. 15B**

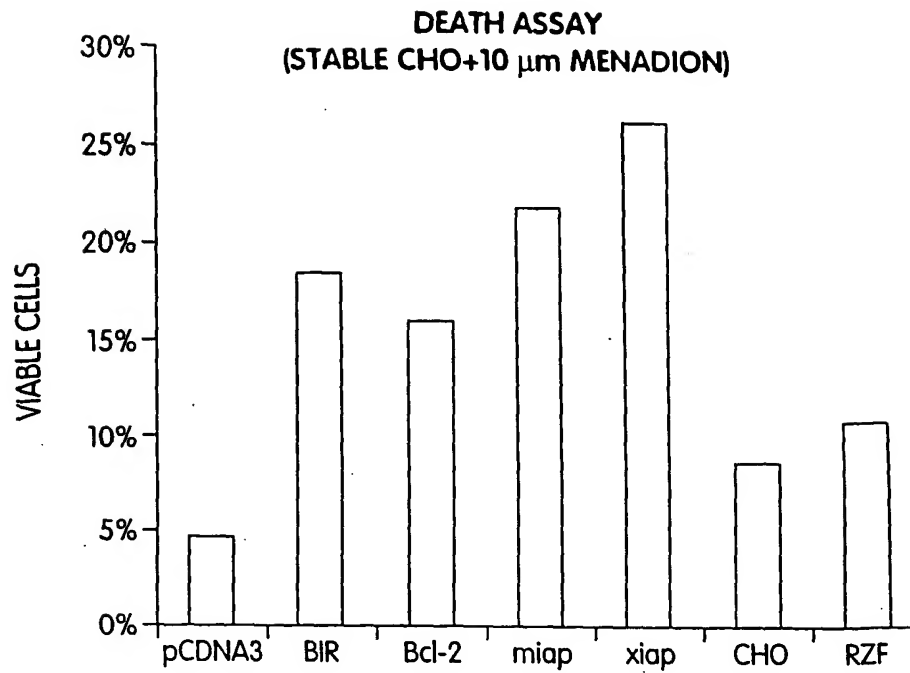


Fig. 16A

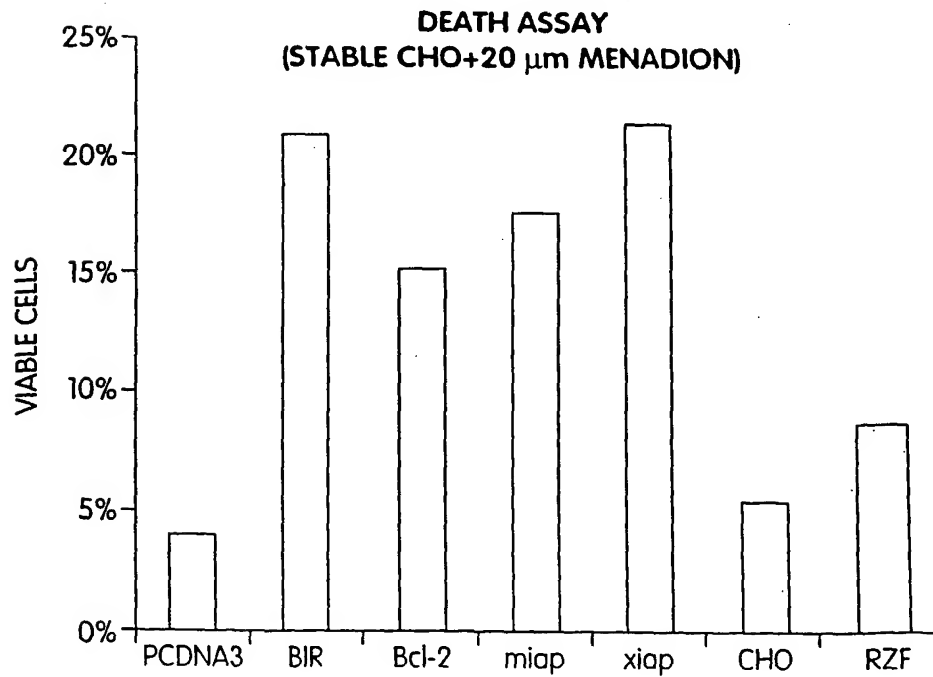


Fig. 16B

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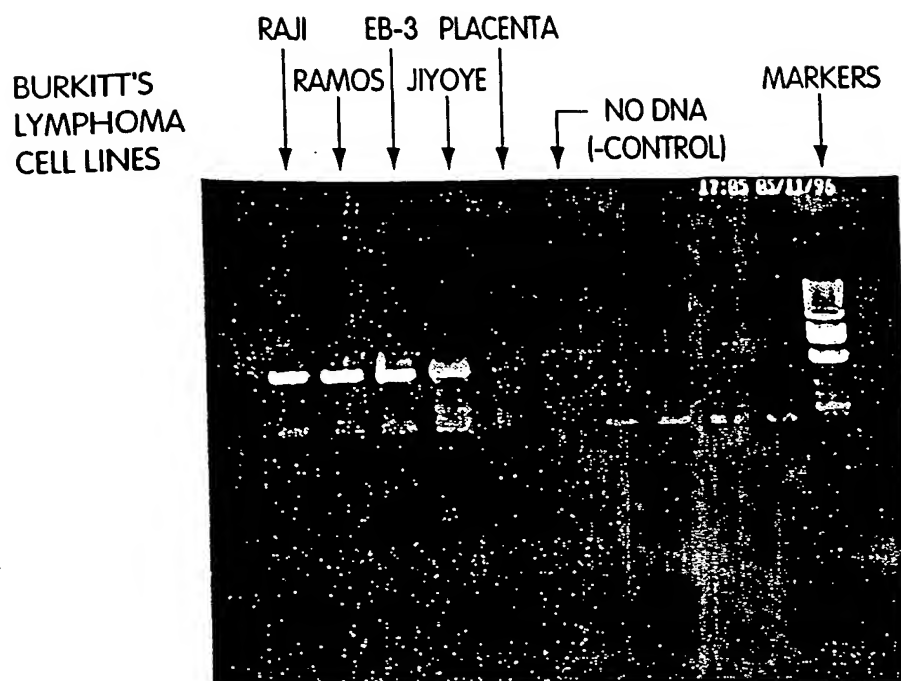


Fig. 17

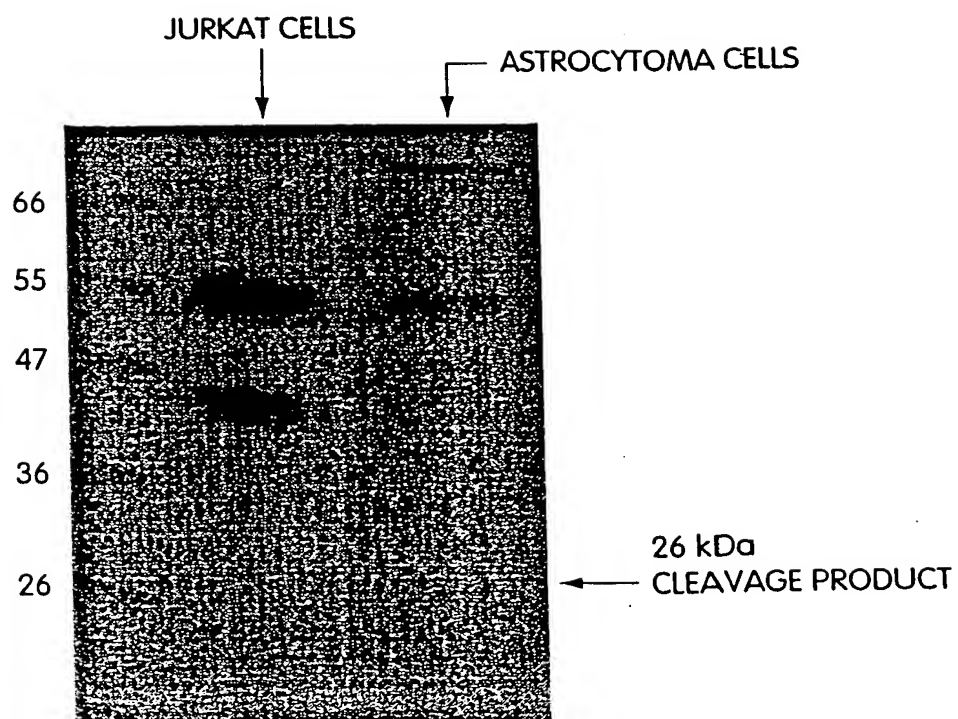


Fig. 18

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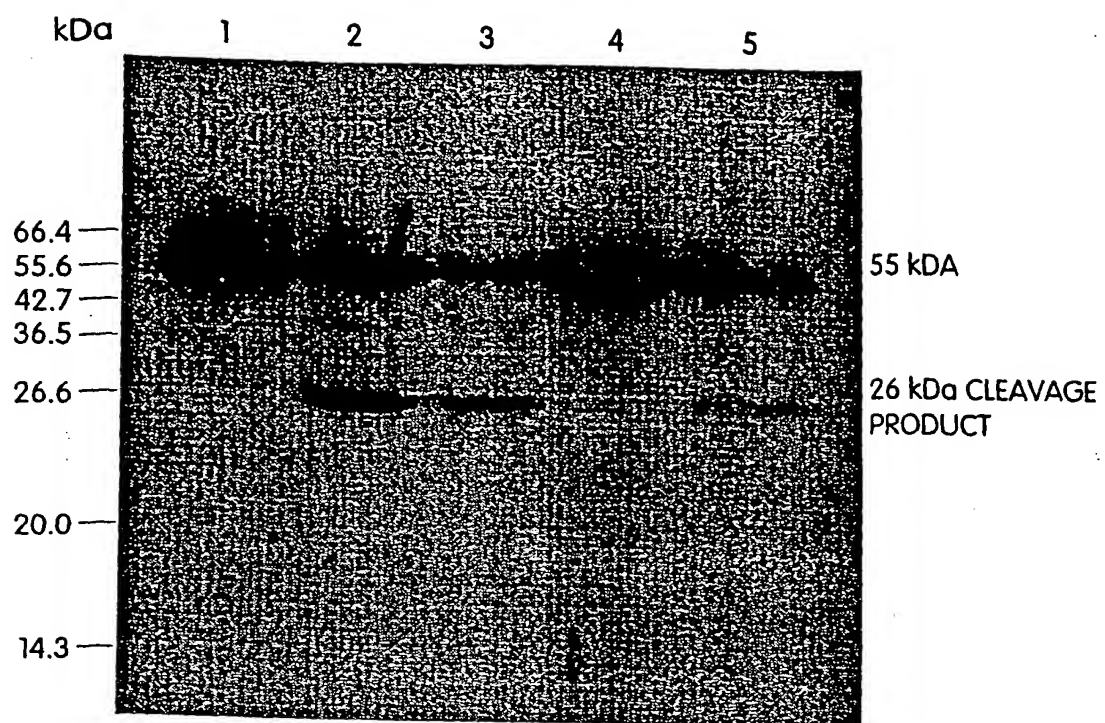


Fig. 19

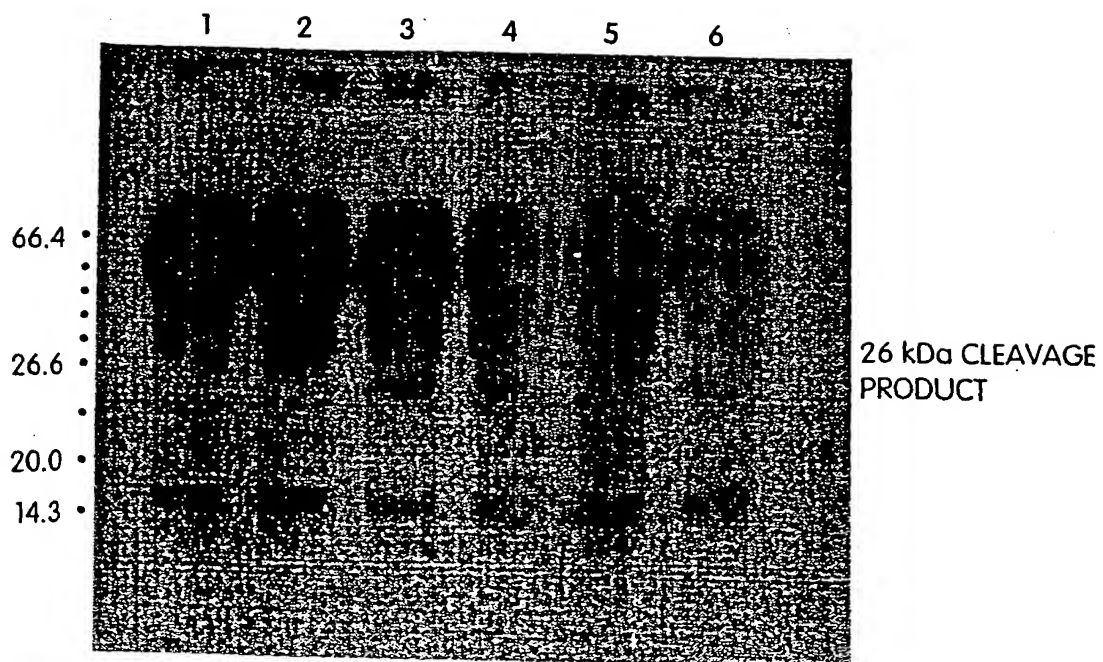


Fig. 20

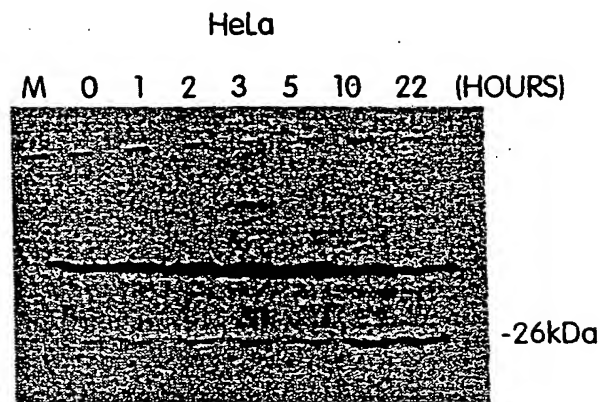


Fig. 21A

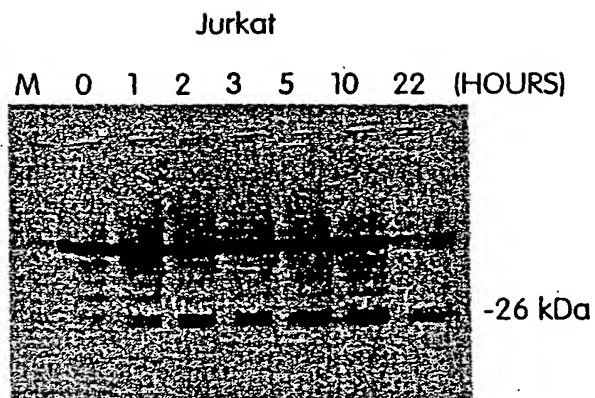


Fig. 21B

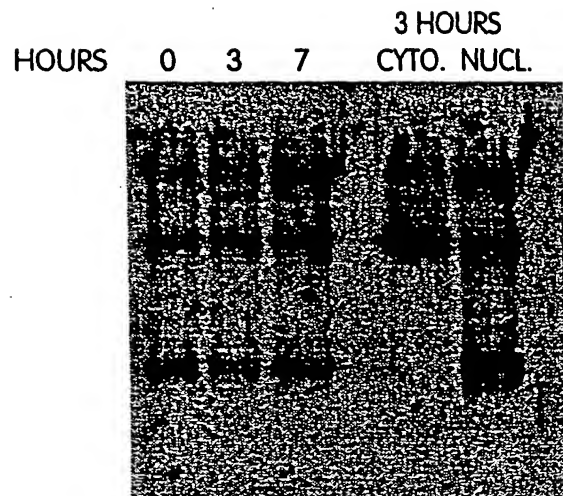


Fig. 22A

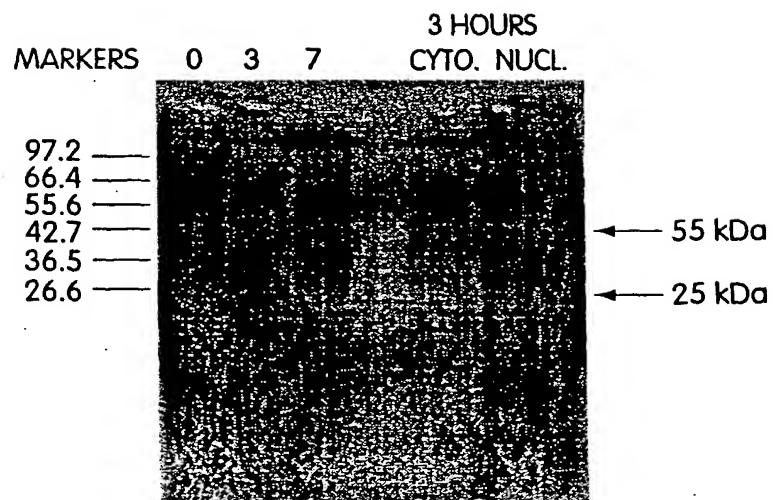


Fig. 22B

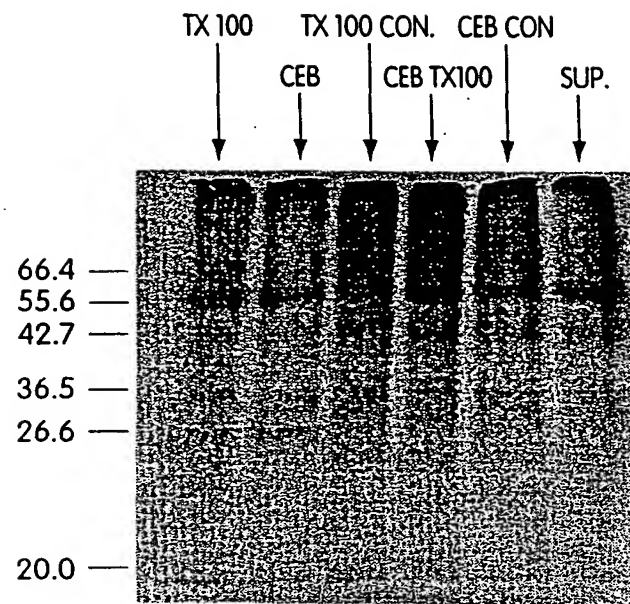


Fig. 23